

From: Whiteman, Brian
Sent: Monday, August 29, 2005 4:04 PM
To: STIC-Biotech/ChemLib
Subject: seq search

09/801,371

SEQ ID NO: 1 and 2

1) the commercial databases, and the issued and published US application databases

Thank you,

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 9/1/05
Date Completed: 9/14/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 2 AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 0311
WWW/Internet: _____
Other(Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6

Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:55:28 ; Search time 1896.05 Seconds
(without alignments)
2657.805 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggctcc.....ggttctgcccagaatgtgc 104

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	400	11	GI3533 SHGC-11076
2	104	100.0	787	6	BD137681 Self-regu
3	104	100.0	787	6	AR300453 Sequence
4	104	100.0	787	6	BD070551 Self-regu
5	104	100.0	1275	6	I08430 Sequence 5
6	104	100.0	1323	6	I07953 Sequence 6
7	104	100.0	1324	6	E00702 cDNA encodi
8	104	100.0	1324	6	I03610 Sequence 2
9	104	100.0	1465	6	I04244 Sequence 2
10	104	100.0	1585	6	A37272 Sequence 12
11	104	100.0	1585	6	I04169 Sequence 1
12	104	100.0	1585	6	I04198 Sequence 1
13	104	100.0	1585	6	I08384 Sequence 5
14	104	100.0	1585	6	I08429 Sequence 3
15	104	100.0	1585	6	AR380784 Sequence
16	104	100.0	1585	9	HUMTNFAA
17	104	100.0	1606	6	I07541
18	104	100.0	1643	6	AR146199 Sequence
19	104	100.0	1643	6	AR366225 Sequence

20	104	100.0	1643	9	HSTNER	X01394 Human mRNA
21	104	100.0	1676	9	BC028148	BC028148 Homo sapi
22	104	100.0	2270	6	BD137687	BD137687 Self-regu
23	104	100.0	2270	6	AR300459	AR300459 Sequence
24	104	100.0	2570	6	BD137688	BD137688 Self-regu
25	104	100.0	2570	6	AR300460	AR300460 Sequence
26	104	100.0	3103	9	HUMTNFX	M26331 Human tumor
27	104	100.0	3634	6	AR100270	AR100270 Sequence
28	104	100.0	3634	6	AR149925	AR149925 Sequence
29	104	100.0	3634	6	BD227798	BD227798 Antisense
30	104	100.0	3634	6	BD271232	BD271232 Predictio
31	104	100.0	3634	6	BD064008	BD064008 Novel exp
32	104	100.0	3634	9	HSTNEA	X02910 Human gene
33	104	100.0	4830	9	AY066019	AY066019 Homo sapi
34	104	100.0	6974	9	AB088112	AB088112 Homo sapi
35	104	100.0	7112	6	AX100950	AX100950 Sequence
36	104	100.0	7112	6	AX100965	AX100965 Sequence
37	104	100.0	7112	9	HUMTNFAB	M15441 Human tumor
38	104	100.0	7240	9	AY214167	AY214167 Homo sapi
C 39	104	100.0	10728	6	AR562497	AR562497 Sequence
C 40	104	100.0	16310	9	HSTNFABX	Z15026 Homo sapien
41	104	100.0	40160	9	BX248519	BX248519 Human DNA
42	104	100.0	61358	9	AL929587	AL929587 Human DNA
C 43	104	100.0	81800	9	HSY14768	Y14768 Homo sapien
C 44	104	100.0	100000	9	AP000505	AP000505 Homo sapi
45	104	100.0	100409	9	BX927320	BX927320 Human DNA

ALIGNMENTS

RESULT 1

GI3533

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

GI3533 SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
400 bp DNA linear STS 30-MAR-2000

GI3533

GI3533.1

GI:1129272

STS

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)

Olivier, M. and Cox, D.R.

Unpublished, Olivier, M., Cox, D.R. (2000)

Unpublished (2000)

Contact: Michael Olivier, David R. Cox

Stanford Human Genome Center

Stanford University School of Medicine

4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA

Tel: (650) 320-5800

Fax: (650) 320-5801

Email: olivier@shgc.stanford.edu

Primer A: CACTAAGAATTCAACTGGGC

Primer B: GAGTAAGGCTAAGTCCAC

STS size: 166

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

Db	222	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGATCCCTGACATCTG	281
Qy	61	GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	104
Db	282	GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	325
RESULT 3			
AR300453			
LOCUS			
DEFINITION Sequence 7 from patent US 6537784.			
ACCESSION AR300453			
VERSION AR300453.1 GI:31687895			
KEYWORDS			
SOURCE Unknown.			
ORGANISM			
Unclassified.			
REFERENCE			
1 (bases 1 to 787)			
AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.			
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy			
JOURNAL Patent: US 6537784-A 7 25-MAR-2003;			
FEATURES			
Location/Qualifiers			
source			
1..787			
/organism="unknown"			
/mol_type="genomic DNA"			
ORIGIN			
Query Match 100.0%; Score 104; DB 6; Length 787;			
Best Local Similarity 100.0%; Pred. No. 1.3e-24;			
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGATCCCTGACATCTG	60
Db	222	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGATCCCTGACATCTG	281
Qy	61	GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	104
Db	282	GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	325
RESULT 4			
BD070551			
LOCUS			
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.			
ACCESSION BD070551			
VERSION BD070551.1 GI:22616154			
KEYWORDS JP 2001516210-A/13.			
SOURCE unidentified			
ORGANISM			
unclassified.			
1 (bases 1 to 787)			
AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.			
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy			
JOURNAL Patent: JP 2001516210-A 13 25-SEP-2001;			
BOEHRINGER INGELHEIM PHARMACEUTICALS INC			
OS Unidentified			
PN JP 2001516210-A/13			
PD 25-SEP-2001			
PF 27-FEB-1998 JP 1998537909			
PI 28-FEB-1997 US 60/032666			
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC			
A61K31/70,C07H21/04,C12N15/12,C12P19/34			
CC Strandedness: Single;			
CC Topology: Linear;			
CC TNF alpha nontranslated region			
FH Key Location/Qualifiers			
FT source			
1..787			
/organism="Unidentified".			
FEATURES			
Location/Qualifiers			
source			
1..787			
/organism="unidentified"			
/mol_type="genomic DNA"			
ORIGIN			
Query Match 100.0%; Score 104; DB 6; Length 787;			
Best Local Similarity 100.0%; Pred. No. 1.3e-24;			
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGATCCCTGACATCTG	60

```
ORIGIN
/db_xref="taxon:32644"
Query Match 100.0%; Score 104; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 750 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 809

Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 810 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 853

RESULT 7
E00702
LOCUS E00702 1324 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human tumor necrosis factor.
ACCESSION E00702
VERSION E00702.1 GI:2168979
KEYWORDS JP 1986040221-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.
TITLE TUMOR NECROTIC FACTOR
JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;
GENENTECH INC
COMMENT OS homosaapiens
PN JP 1986040221-A/1
PD 26-FEB-1986
PF 05-JUL-1985 JP 1985149075
PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR
05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR
03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454, PI BARAA
BUSHIYAN AGAARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HII RII,
PI GUREN EBAN NEDOUIN
PC A61K35/12,A61K35/02,A61K35/14,A61K35/74,A61K37/04,C07H21/02,
PC C07H21/04,
PC C12N15/00;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell type=promyelocytes;
CC *source: cell_line=HL-60;
CC *source: clone=lamda42-4, lamda16-4;
CC Key Location/Qualifiers
FH sig_peptide <1..61
FT mat_peptide 62..532
FT /product='tumor necrosis factor' FT CDS
FT <1..535 /product='tumor necrosis factor' FT 3'UTR
FT 536..>1324.
FEATURES
source Location/Qualifiers
1..1324
/organism="Homo sapiens"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 810

Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 811 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 854
```

```
ORIGIN
/db_xref="taxon:32644"
Query Match 100.0%; Score 104; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281

Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 282 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 325

RESULT 5
I08430
LOCUS I08430 1275 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8604606.
ACCESSION I08430
VERSION I08430.1 GI:588860
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED PROTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR
JOURNAL Patent: WO 8604606-A 5 14-AUG-1986;
FEATURES Location/Qualifiers
source 1..1275
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 693 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 752

Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 753 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 796

RESULT 6
I07953
LOCUS I07953 1323 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0168214.
ACCESSION I07953
VERSION I07953.1 GI:589335
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1323)
AUTHORS Aggarwal,B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
TITLE Tumor necrosis factor, methods for its preparation, compositions
containing it, DNA encoding it and assay method using such DNA
JOURNAL Patent: EP 0168214-A2 6 15-JAN-1986;
FEATURES Location/Qualifiers
source 1..1323
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1323;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
```

RESULT 8
LOCUS I03610 1324 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4650674.
ACCESSION I03610
VERSION I03610.1 GI:268632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Agarwal B.B. and Lee, S. He.
TITLE Synergistic cytotoxic composition
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, CA
FEATURES
source
1..1324
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 751 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810
Qy 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 811 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854
RESULT 9
LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION I04244
VERSION I04244.1 GI:268725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Lin, L.S. and Yamamoto, R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source
1..1465
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 883 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 942
Qy 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 943 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 986
RESULT 10
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.

ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1585)
AUTHORS Vile, R.G. and Hart, I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
FEATURES
source
1..1585
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106
RESULT 11
LOCUS I04169 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677063.
ACCESSION I04169
VERSION I04169.1 GI:268716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark, D.F., Wang, A.M., Ladner, M.B., Creasey, A.A., Lin, L.S. and Van Arsdell, J.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source
1..1585
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACCTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106
RESULT 12
LOCUS I04198 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677064.
ACCESSION I04198
VERSION I04198.1 GI:268719
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdel,J.N. and Lin,L.S.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source
1..1585
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1106
RESULT 13
108384
LOCUS I08384 1585 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION I08384
VERSION I08384.1 GI:588904
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van Arsdel,J.N.
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
FEATURES
source
1..1585
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1106
RESULT 14
108429
LOCUS I08429 1585 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8604606.
ACCESSION I08429
VERSION I08429.1 GI:588859
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1585)

AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 3 14-AUG-1986;
FEATURES
source
1..1585
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1106
RESULT 15
AR380784
LOCUS AR380784 1585 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1329 from patent US 6607879.
ACCESSION AR380784
VERSION AR380784.1 GI:40088418
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1329 19-AUG-2003;
FEATURES
source
1..1585
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1106
Search completed: September 3, 2005, 01:14:20
Job time : 1902.05 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:45:43 ; Search time 319.075 Seconds
(without alignments)
1929.494 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggctcc.....ggttctggccagaatgtgc 104

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	104	3	Aaz99816 Cis-actin
2	104	100.0	787	2	Aaz20979 Human TNF
3	104	100.0	792	13	Adr12297 Human tum
4	104	100.0	1275	1	Aan60558 Sequence
5	104	100.0	1323	1	Aan60363 Sequence
6	104	100.0	1324	3	Aaa34963 Human ade
7	104	100.0	1324	3	Aaf21085 Human low
8	104	100.0	1324	10	Abz96779 Human nuc
9	104	100.0	1324	11	Abd20628 Human pul
10	104	100.0	1560	1	Aan80219 Sequence
11	104	100.0	1581	12	Adq83817 Human tum
12	104	100.0	1585	1	Aan60557 Sequence
13	104	100.0	1585	8	Acab4836 Human TNF
14	104	100.0	1585	10	Adf76346 Novel hum
15	104	100.0	1585	11	Adi32003 Human cdn
16	104	100.0	1585	12	Ado19587 Human PRO
17	104	100.0	1585	13	Adr24640 Breast ca
18	104	100.0	1585	13	Adp54654 Human PRO
19	104	100.0	1606	1	Aan60446 Sequence
20	104	100.0	1606	2	Aat15424 Human tum

21	104	100.0	1643	2	AAT31021	Aat31021 Human tum
22	104	100.0	1643	6	ABK13195	Abk13195 Human tum
23	104	100.0	1643	8	AA153712	Aa153712 Tumour ne
24	104	100.0	1643	8	AA49644	Aad49644 Human tum
25	104	100.0	1643	10	ADC35185	Adc35185 Human CDN
26	104	100.0	1643	10	AA83904	Aad63904 Human TNF
27	104	100.0	1643	10	ACC57575	Acc57575 Polynucle
28	104	100.0	1643	13	ADR26040	Adr26040 Breast ca
29	104	100.0	1650	8	ACF64375	Acf64375 Human TNF
30	104	100.0	1666	10	ADE25664	Ade25664 Human cDN
31	104	100.0	1669	13	ADS88038	Ad888038 Tumour tr
32	104	100.0	1669	13	ADT08160	Adt08160 Human tum
33	104	100.0	2270	2	AAZ20983	Aaz20983 ChimERIC
34	104	100.0	2570	2	AAZ20984	Aaz20984 ChimERIC
35	104	100.0	3634	2	AAV39005	Aav39005 TNF-alpha
36	104	100.0	3634	2	AAx09014	Aax09014 Tumour ne
37	104	100.0	3634	3	AAA40760	Aaa40760 Human tum
38	104	100.0	3634	3	AAc63770	Aac63770 Human TNF
39	104	100.0	3634	8	ACC57891	Acc57891 Human tum
40	104	100.0	3634	8	ACA64946	Ac64946 Human TNF
41	104	100.0	3634	9	ACD04988	Ac04988 DNA encod
42	104	100.0	3634	10	ACF63382	Acf63382 Human TNF
43	104	100.0	3634	12	ADQ29070	Adq29070 Human tum
44	104	100.0	3634	13	ADR02586	Adr02586 Human tum
45	104	100.0	4830	12	ACF57523	Acf57523 Human TNF

ALIGNMENTS

RESULT 1

AAZ99816

ID AAZ99816 standard; RNA; 104 BP.

XX

AC AAZ99816;

XX

DT 12-JUL-2000 (first entry)

XX

DE Cis-acting nucleotide sequence derived from human TNF-alpha.

XX

KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;

KW RNA-activated protein kinase; eukaryotic initiation factor 2; eif2alpha;

KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200014255-A1.

XX

PD 16-MAR-2000.

XX

PF 06-SEP-1999; 99WO-IL0000483.

XX

PR 07-SEP-1998; 98IL-00126112.

PR

26-OCT-1998; 98IL-00126757.

XX

(YISS) YISSUM RES & DEV CO.

XX

Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX

WPI; 2000-257000/22.

DR

Regulation of gene expression by mRNA splicing is carried out using a cis

-acting nucleotide sequence controlled by phosphorylation of the alpha-

subunit of eukaryotic initiation factor 2.

XX

Claim 4; Page 15; 75pp; English.

PS

The specification describes a cis-acting nucleotide sequence which is

capable of removing introns from a precursor transcript encoded by a gene

which harbours at least one cis-acting nucleotide sequence. This removal

is effected during the production of mRNA of the gene, and depends on

activation of a trans-acting factor which is an RNA-activated protein

kinase capable of phosphorylating the alpha-subunit of eukaryotic

CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
 CC sequence, derived from the 3' untranslated region (3'UTR) of the human
 CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
 CC splicing of precursor transcripts encoded by that gene sensitive to the
 CC level of RNA-activated protein kinase (PKR) activity. The sequence can be
 CC used to transform host cells to regulate gene expression at the mRNA
 CC splicing level, for gene therapy, and to produce a recombinant
 CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
 CC protein) or industrially or agriculturally applicable protein. The
 CC present sequence represents a cis-acting nucleotide sequence of the
 CC invention

XX
 SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 3; Length 104;
 Best Local Similarity 100.0%; Pred. No. 3.1e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
 Db 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
 Qy 61 GAATCTGGAGACACAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
 Db 61 GAATCTGGAGACACAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104

RESULT 2
 ID AA220979 standard; DNA; 787 BP.
 XX
 AC AA220979;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human TNFalpha 3'UTR.
 XX
 KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
 KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
 KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
 KW ankylosing spondylitis; rheumatoid arthritis; ds.

OS Homo sapiens.
 XX
 FN WO9943840-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 12-JAN-1999; 99WO-US000637.
 XX
 PR 27-FEB-1998; 98US-0076316P.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Tatake RJ, Marlin SD, Barton RW;
 XX
 DR WPI; 1999-527630/44.
 XX

XX A chimeric polynucleotide consisting of a tissue necrosis factor (TNF)
 XX promoter and an apoptosis-inducing Granzyme B polynucleotide.

XX Example 1; Page 60-61; 71pp; English.

XX This sequence represents a human TNFalpha (tumour necrosis factor alpha)
 CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
 CC constructed comprising at least one TNFalpha promoter enhancer region
 CC (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA encoding
 CC the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha
 CC 3'UTR sequence. TNFalpha is one of a number of cytokines produced by
 CC inflammatory cells. Upregulation and/or dysregulation of cytokines in
 CC inflamed tissue may be directly or indirectly responsible for
 CC exacerbation of chronic inflammatory diseases. Introduction of the
 CC chimeric nucleotide to activated inflammatory cells causes them to

CC undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide
 CC may be useful for treating inflammatory disorders such as multiple
 CC sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus
 CC host disease, lupus erythematosus, insulin-dependent (type I) diabetes
 CC mellitus, ankylosing spondylitis, and in particular, rheumatoid
 CC arthritis. The use of such chimeric nucleotides offers simpler and
 CC cheaper long-term relief, in comparison with existing conventional
 CC pharmaceutical and invasive surgery methods

XX
 SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 2; Length 787;
 Best Local Similarity 100.0%; Pred. No. 5.4e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
 Db 222 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281
 Qy 61 GAATCTGGAGACACAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
 Db 282 GAATCTGGAGACACAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 325

RESULT 3
 ADR12297
 ID ADR12297 standard; DNA; 792 BP.
 XX
 AC ADR12297;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human tumour necrosis factor alpha 3'-untranslated region DNA.
 XX
 KW ss; cytostatic; VEGF modulator; angiogenesis inhibitor;
 KW UTR-dependent expression; vascular endothelial growth factor;
 KW untranslated region; cancer; angiogenesis.

OS Homo sapiens.
 XX
 FN WO2004065561-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 21-JAN-2004; 2004WO-US001643.
 XX
 PR 21-JAN-2003; 2003US-0441637P.
 XX
 PA (PTCT-) PTC THERAPEUTICS INC.
 XX
 PI Cao L, Trifillis P;
 XX
 DR WPI; 2004-571681/55.
 XX
 PT Identifying modulators of untranslated region-dependent expression of a
 XX VEGF gene, useful for treating cancer, comprises contacting a compound
 XX with a cell or translation mixture containing a reporter gene linked to a
 XX VEGF gene UTR.

XX Example; SEQ ID NO 6; 251pp; English.

XX A method of identifying (M1) a compound that modulates untranslated
 CC region-dependent expression of a vascular endothelial growth factor
 CC (VEGF) gene comprises contacting a member of a library of compounds with
 CC a cell or cell-free translation mixture containing a reporter gene
 CC operably linked to an untranslated region (UTR) of the VEGF gene, and
 CC detecting expression of the reporter gene. A compound is identified as
 CC modulator if the level of expression of the reporter gene in the presence
 CC of the compound is altered as compared to that in the absence of the
 CC compound or in the presence of a control. Compounds identified by M1 are
 CC useful for treating, preventing or ameliorating cancer or its symptoms,
 CC and/or for inhibiting angiogenesis. This sequence corresponds to a
 CC therapeutic untranslated region used in the invention.

SQ Sequence 792 BP; 192 A; 203 C; 172 G; 225 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 13; Length 792;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
219 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 278
QY 61 GAATCTGGAGACAGGAGCCTTGGTTCTTGCCAGAAATGCTGC 104
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
279 GAATCTGGAGACAGGAGCCTTGGTTCTTGCCAGAAATGCTGC 322

RESULT 4
AAN60558
ID AAN60558 standard; DNA; 1275 BP.
XX AC AAN60558;
XX DT 28-JUL-1991 (first entry)
XX DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
DE 69 in pAW731.
XX KW Antitumour; anticancer; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1..474
FT /*tag= a
XX WO8604606-A.
XX PD 14-AUG-1986.
XX PF 03-FEB-1986; 86WO-US000236.
XX PR 07-FEB-1985; 85US-00698939.
XX PA (CETU) CETUS CORP.
XX PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX WPI; 1986-225458/34.
XX P-PSDB; AAP60656.
XX New synthetic muteins of human tumour necrosis factor protein - are obtd.
XX by direct mutagenesis and retain antitumour activity.
XX Disclosure; Fig 3a; 47pp; English.
XX The sequence encoding TNF produced by the promyelocytic leukemia cell
CC line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see
CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
CC sequence appears to be involved in disulphide linkages. The patentors
CC claim a novel synthetic mutein of a biologically active hTNF protein,
CC having at least one cysteine residue free from a disulphide link and non-
CC essential to the activity and having at least one of the cysteine
CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC claimed
XX SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 693 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 752
QY 61 GAATCTGGAGACAGGAGCCTTGGTTCTTGCCAGAAATGCTGC 104
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
753 GAATCTGGAGACAGGAGCCTTGGTTCTTGCCAGAAATGCTGC 796

RESULT 5
AAN60363
ID AAN60363 standard; DNA; 1323 BP.
XX AC AAN60363;
XX DT 19-JUN-1991 (first entry)
XX DE Sequence encoding human tumour necrosis factor.
XX KW hTNF; tumour; cancer; interferon; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1..534
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..534
FT /*tag= c
XX BP168214-A.
XX PD 15-JAN-1986.
XX PF 03-JUL-1985; 85EP-00304758.
XX PR 05-JUL-1984; 84US-00627959.
XX PR 05-JUL-1984; 84US-00628059.
XX PR 05-JUL-1984; 84US-00628060.
XX PR 03-DEC-1984; 84US-00677156.
XX PR 03-DEC-1984; 84US-00677257.
XX PR 03-DEC-1984; 84US-00677267.
XX PR 03-DEC-1984; 84US-00677454.
XX PA (GETH) GENENTECH INC.
XX PI Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;
XX WPI; 1986-015483/03.
XX P-PSDB; AAP60417.
XX Pure tumour necrosis factor and mutant forms - new DNA coding sequences
XX and transformed cells.
XX Claim 20; Fig 10; 90pp; English.
XX Sequence encodes the pure human tumour necrosis factor, mutants of which
CC are covered by the claims. TNF and mutants are useful in treating
CC tumours, especially in tandem with interferon. The encoding sequence may
CC be used to create plasmid pTRXAPTNP, allowing transformation of an
CC E.coli host for the expression of TNF
XX SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 1; Length 1323;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
750 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 809
QY 61 GAATCTGGAGACAGGAGCCTTGGTTCTTGCCAGAAATGCTGC 104

Db 810 GAATCTGGAGACGAGGACCTTTGGTCTTGGCCGAGATGCTGC 853
|||||
Query Match 100.0%; Score 104; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. NO. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 6
ID AAA34963
XX AAA34963 standard; DNA; 1324 BP.
AC AAA34963;
XX 28-JUL-2000 (first entry)
XX Human adenosine receptor related polynucleotide SEQ ID NO:2652.
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
XX WO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99US-05017712.
XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX Nyce JW;
XX WPI; 2000-205971/18.
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX Disclosure; Page 814-815; 1343pp; English.
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3323 to
CC AAA3392) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. NO. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 7
ID AAF21085 standard; DNA; 1324 BP.
XX AAF21085;
AC AAF21085;
XX 14-MAR-2001 (first entry)
XX Human low adenosine antisense oligonucleotide related sequence #2652.
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX Homo sapiens.
XX WO200062736-A2.
XX 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US008020.
XX 06-APR-1999; 99US-0127958P.
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX Nyce JW;
XX WPI; 2000-679539/66.
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX Disclosure; Page 887; 1592pp; English.
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide

transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
751 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

61 GAATCTGAGACACAGGGAGCCTTTGGTTCTGSCCAGAAATGCTGC 104

811 GAATCTGAGACACAGGGAGCCTTTGGTTCTGSCCAGAAATGCTGC 854

RESULT 8

ABZ96779

ID ABZ96779 standard; DNA; 1324 BP.

AC ABZ96779;

17-OCT-2003 (first entry)

Human nucleic acid sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.

Disclosure; SEQ ID NO 12021; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the

initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 10; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60

751 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

61 GAATCTGAGACACAGGGAGCCTTTGGTTCTGSCCAGAAATGCTGC 104

811 GAATCTGAGACACAGGGAGCCTTTGGTTCTGSCCAGAAATGCTGC 854

RESULT 9

ABD20628

ID ABD20628 standard; DNA; 1324 BP.

AC ABD20628;

29-JUL-2004 (first entry)

Human pulmonary and inflammatory target DNA #239.

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
respiratory tract inflammation; adenosine sensitivity; lung; cancer;
surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
pulmonary transplantation rejection; ds.

Homo sapiens.

WO200285309-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;

WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense
oligonucleotide containing less percentage of adenosine, targeted to
nucleic acids associated with lung airway or lung dysfunction, and

```

PT bronchodilating agent.
XX Claim 15; SEQ ID NO 12021; 763pp; English.
PS This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match      100.0%; Score 104; DB 11; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db      751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

Qy      61  GAATCTGGAGACCCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
Db      811 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 854

RESULT 10
AA80219
ID  AA80219 standard; DNA; 1560 BP.
AC  AA80219;
XX
XX 28-DEC-1990 (first entry)
XX
XX Sequence of pE4 encoding human tumour necrosis factor (TNF).
XX Lymphokine; antitumour; ss.
XX Homo sapiens.
XX
XX Key      Location/Qualifiers
XX FT      86..313
XX CDS      /*tag= a
XX FT      314..787
XX mat_peptide /*tag= b
XX
XX WO8806625-A.
XX
XX 07-SEP-1988.

```

```

XX 25-JAN-1988; 88WO-US000183.
PF
XX 26-FEB-1987; 87US-00019221.
PR
XX (CETU ) CETUS CORP.
PA
XX Mark DF, Lin LS, Thomson JW, Yamamoto R;
PI
XX WPI; 1988-271165/38.
DR
XX P-PSDB; AAP80728.
DR
XX Human tumour necrosis factor muteins - having comparable biological
PT activity with improved stability and ease of purification.
PS
XX Disclosure; Fig 1-1 to 1-2; 51pp; English.
XX
XX A human TNF protein which is modified from the sequence shown in
CC AAP80728, including naturally occurring allelic variants is claimed. Also
CC claimed are: recombinant DNA sequences encoding the protein (AA80219)
CC and control sequences for expression; a vector; a transformed host cell;
CC a method of producing the protein by culturing the host cell;
CC pharmaceutical compen. of the protein and a carrier and a method of
CC treating tumour burden with the compen. The muteins are capable of the
CC range of biological activities exhibited by native TNF but exhibit
CC improved stability and ease of purification
XX
SQ Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 U; 0 Other;

Query Match      100.0%; Score 104; DB 1; Length 1560;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db      1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy      61  GAATCTGGAGACCCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
Db      1063 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 1106

RESULT 11
ADQ83817
ID  ADQ83817 standard; cDNA; 1581 BP.
XX
XX AC  ADQ83817;
XX
XX 07-OCT-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #631.
DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX
XX WO2004060270-A2.
XX
XX 22-JUL-2004.
XX
XX 15-OCT-2003; 2003WO-US029126.
XX
XX 18-OCT-2002; 2002US-0418988P.
XX
XX (GETH ) GENENTECH INC.
XX PA (WUTD/) WU T D.
XX PA (ZHOU/) ZHOU Y.
XX
XX Wu TD, Zhou Y;
XX
XX WPI; 2004-534300/51.
XX

```

PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 631; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 1581 BP; 351 A; 471 C; 385 G; 374 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 12; Length 1581;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 60
DB 999 GAATTCAGGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 1058

QY 61 GAATTCGAGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 104
DB 1059 GAATTCGAGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 1102

RESULT 12
AAN60557
ID AAN60557 standard; DNA; 1585 BP.
XX
XX AAN60557;
XX
DT 28-JUL-1991 (first entry)
XX
DE Sequence encoding mature human tumour necrosis factor (htnf) in pE4.
XX
KW Antitumour; anticancer; ss.
XX
XX Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 86..313
FT mat_peptide /*tag= a
FT 314..787
FT /*tag= b
XX
PN WO8604606-A.
XX
PD 14-AUG-1986.
XX
PF 03-FEB-1986; 86WO-US000236.
XX
PR 07-FEB-1985; 85US-00698939.
XX
PA (CETU) CETUS CORP.
XX
PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR WPI; 1986-225458/34.
XX
DR P-PSDB; AAP60655.
XX
PT New synthetic muteins of human tumour necrosis factor protein - are obt'd.
PT by direct mutagenesis and retain antitumour activity.
XX
PS Disclosure; Fig 1; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia cell
CC line (HL-60, ATCC no CCL240) has been cloned and expressed in E.coli (see
CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
CC sequence appears to be involved in disulphide linkages. The patentors
CC claim a novel synthetic mutein of a biologically active hTNF protein,
CC having at least one cysteine residue free from a disulphide link and non-
CC essential to the activity and having at least one of the cysteine
CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC claimed
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 1; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAGGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATTCGAGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 104
DB 1063 GAATTCGAGACCGAGGCGCTTGGTCTGCGGCGCTACAGCTTTGATCCCTGACATCTG 1106

RESULT 13
ACA64836
ID ACA64836 standard; DNA; 1585 BP.
XX
XX ACA64836;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human TNF-alpha DNA corresponding to M10988.
XX
KW Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.
XX
OS Homo sapiens.
XX
PN DE10127572-A1.
XX
PD 05-DEC-2002.
XX
XX 30-MAY-2001; 2001DE-01027572.
XX

```
PR 30-MAY-2001; 2001DE-01027572.
XX (PATH-) PATHOARRAY GMBH.
XX Haeupl T, Ungethuen U, Blaess S;
XX WPI; 2003-240797/24.
XX
XX Reagents for diagnosis, study and therapy of chronic inflammatory joint
XX PT and other diseases, comprises any of many specified genes or derived
XX PT proteins.
XX
XX Claim 1; Page; 12pp; German.
XX
XX This invention describes a novel reagent for diagnosis, molecular
XX CC definition and therapy of chronic inflammatory joint diseases, and other
XX CC inflammatory disorders, infective or tumour diseases in humans. The
XX CC products of the invention have anti-inflammatory, cytostatic,
XX CC antiarthritic, antirheumatic and immunosuppressive activity and can be
XX CC used for gene therapy. The reagent of the invention and any proteins and
XX CC antibodies derived from it, are used (i) for analysing tissue and blood
XX CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
XX CC chronic joint diseases, on the basis of molecular characterisation, and
XX CC determining the etiological pathogenicity principle of as yet
XX CC uncharacterised inflammatory diseases, also monitoring progression and/or
XX CC treatment of disease, and optimisation of therapy and (iii) for
XX CC developing treatments for inflammatory diseases, particularly of joints,
XX CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides
XX CC used in the method of the invention
XX
XX Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 104; DB 8; Length 1585;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-25;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
XX DB 1003 GAATTCAACTGGGGCCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 1062
XX
XX QY 61 GAATCTGGAGACACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
XX DB 1063 GAATCTGGAGACACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1106
XX
XX RESULT 14
XX ID ADF76346
XX ADP76346 standard; cDNA; 1585 BP.
XX
XX AC ADF76346;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Novel human secreted and transmembrane protein cDNA SeqID 19.
XX
XX KW human; PRO; membrane bound protein; membrane bound receptor;
XX KW cell proliferation; cell migration; cell differentiation;
XX KW mitogenic factor; survival factor; cytotoxic factor;
XX KW differentiation factor; neuroptide; hormone; cell receptor;
XX KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
XX OS Homo sapiens.
XX
XX KW Crohn's disease; asthma; ulcerative colitis; hypersensinophilia;
XX KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
XX KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN US6607879-B1.
XX
XX PD 19-AUG-2003.
XX
XX PF 09-FEB-1998; 98US-00023655.
XX

PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
XX WPI; 2003-721702/68.
XX P-PSDB; ADF76347.
XX
XX New PRO polypeptides, useful for diagnosing and treating an immune
XX PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
XX PT diabetes mellitus.
XX
XX Claim 2; SEQ ID NO 19; 918pp; English.
XX
XX This invention relates to novel nucleic acids encoding human PRO secreted
XX CC and transmembrane proteins. Extracellular proteins play important roles
XX CC in the formation, differentiation and maintenance of multicellular
XX CC organisms. The fate of many individual cells (for example proliferation,
XX CC migration or differentiation) is typically governed by information
XX CC received from other cells and the immediate environment. The information
XX CC is often transmitted by secreted polypeptides (for example mitogenic
XX CC factors, survival factors, cytotoxic factors, differentiation factors,
XX CC neuropeptides or hormones) which are received and interpreted by diverse
XX CC cell receptors or membrane bound proteins. These membrane bound proteins
XX CC and receptors may be of use as pharmaceutical and diagnostic agents, such
XX CC as in the blocking of receptor-ligand interactions. The current invention
XX CC provides the amino acid sequences of novel human membrane bound receptors
XX CC and proteins, along with the cDNA sequences encoding them. The novel
XX CC proteins of the invention may have cytostatic activities through the
XX CC stimulation of chondrocytes. The nucleic acids of the invention may be
XX CC useful for the manufacture of a medicament for diagnosing or treating a
XX CC tumour in a mammal. In addition, they may be useful for measuring or
XX CC detecting the expression of a tumour associated gene. The present
XX CC sequence is a cDNA sequence which encodes a human PRO protein of the
XX CC invention.
XX
XX Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 104; DB 10; Length 1585;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-25;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
XX DB 1003 GAATTCAACTGGGGCCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 1062
XX
XX QY 61 GAATCTGGAGACACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
XX DB 1063 GAATCTGGAGACACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1106
XX
XX RESULT 15
XX ID ADI32003
XX ADI32003 standard; cDNA; 1585 BP.
XX
XX AC ADI32003;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE Human cDNA #1329.
XX
XX KW Human; gene; ss; immunological response; immunopathological condition;
XX KW Crohn's disease; asthma; ulcerative colitis; hypersensinophilia;
XX KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
XX KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN US6607879-B1.
XX
XX PD 19-AUG-2003.
XX
XX PF 09-FEB-1998; 98US-00023655.
XX
```


XX	
PR	09-FEB-1998; 98US-00023655.
XX	(INCY-) INCYTE CORP.
PA	
XX	Cocks BG, Stuart SG, Seilhamer JJ;
PI	
XX	WPT; 2003-895307/82.
DR	
XX	A composition comprising a plurality of cDNAs, useful for detecting
PT	altered expression of genes in an immunological response or for
PT	diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT	or osteoarthritis.
XX	
PS	Claim 1; SEQ ID NO 1329; 50pp; English.
XX	
CC	The invention relates to a composition comprising a plurality of cDNAs
CC	for detecting the altered expression of genes in an immunological
CC	response. The invention also relates to a method of diagnosing or
CC	monitoring the treatment of an immunopathological condition in a sample,
CC	comprising obtaining nucleic acids from a sample, contacting the nucleic
CC	acids of the sample with an array comprising the plurality of cDNAs under
CC	conditions to form one or more hybridisation complexes, detecting the
CC	hybridisation complexes and comparing the levels of the detected
CC	hybridisation complexes with the level of hybridisation complexes
CC	detected in a non-diseased sample, where an altered level of the detected
CC	hybridisation complexes correlates with the presence of an
CC	immunopathological condition. Also disclosed are an expression profile
CC	comprising a microarray and a plurality of detectable complexes and a
CC	method for identifying a plurality of polynucleotide probes. The cDNAs
CC	are useful as hybridisable array elements in a microarray for monitoring
CC	the expression of target polynucleotides. The microarray can be used in
CC	the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC	ulcerative colitis, hypersplenophilia, irritable bowel syndrome,
CC	osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC	identifying agents for the treatment of the diseases. The microarray may
CC	also be used in drug discovery and development, toxicological and
CC	carcinogenicity studies, forensics or pharmacogenomics. The composition
CC	may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC	genomic fragments. This sequence represents a human cDNA of the
CC	invention. Note: The sequence data for this patent did not form part of
CC	the printed specification but was obtained in electronic format directly
CC	from USPTO at seqdata.uspto.gov/sequence.html.
XX	
SQ	Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
	Query Match 100.0%; Score 104; DB 11; Length 1585;
	Best Local Similarity 100.0%; Pred. No. 6.Se-25;
	Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 GAATTTCAAACCTGGGCGCCTCCAGAACTCACTGGGGCTACAGCTTGATCCTCGCATCTG 60
Dd	1003 GAATTCAAACTGGGCGCCTCCAGAACTCACTGGGGCTACAGCTTGATCCTCGCATCTG 1062
Qy	61 GAATCTGAGACACGAGGAGCCTTGTGGTCTCGGCAGAAATGCTGC 104
Dd	1063 GAATCTGAGACGAGGAGCCTTGTGGTCTCGGCAGAAATGCTGC 1106

Search completed: September 3, 2005, 00:29:34
Job time : 326.075 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 23:36:03 ; Search time 2377.85 Seconds
(without alignments)
1664.816 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggcctcc.....ggttctggccagaatgtgc 104

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	474	5	BX118951
2	104	100.0	630	6	CB528492
3	104	100.0	645	6	CD370363
4	104	100.0	688	6	CD367676
5	104	100.0	696	6	CA307225
6	104	100.0	699	6	CD364761
7	104	100.0	703	6	CD368142
8	104	100.0	713	6	CA308256
9	104	100.0	719	6	CB528694
10	104	100.0	722	5	BQ007008
11	104	100.0	722	6	CA307062
12	104	100.0	722	6	CD364988
13	104	100.0	723	6	CA308777
14	104	100.0	723	6	CD368116
15	104	100.0	724	6	CA309711
16	104	100.0	726	6	CA310368
17	104	100.0	726	6	CD368929
18	104	100.0	742	6	CA309509
19	104	100.0	744	6	CD366187
20	104	100.0	748	6	CA306559
21	104	100.0	1068	1	AL543083
22	103	99.0	248	7	T29839
23	103	99.0	693	6	CD367625
24	102.4	98.5	684	6	CA307429

C 25	102.4	98.5	713	6	CA309664
C 26	102.4	98.5	718	6	CD367794
C 27	100.8	96.9	672	6	CD367664
C 28	92	88.5	755	6	CD240146
C 29	86	82.7	581	1	AI242177
C 30	85	81.7	561	4	BG232086
C 31	68.2	65.6	583	6	CA748748
C 32	61.4	59.0	1011	1	AL575811
C 33	61.2	58.8	564	1	AA699697
C 34	60.8	58.5	562	1	AA207062
C 35	48.2	46.3	546	1	AA824594
C 36	34.8	33.5	136	8	B38591
C 37	32.6	31.3	691	1	AL110410
C 38	32.6	31.3	888	5	BQ232100
C 39	32.2	31.0	342	2	BF407522
C 40	31.8	30.6	876	9	CNS001YJ
C 41	30.6	29.4	652	9	CE210980
C 42	30.6	29.4	701	7	CO049356
C 43	30.6	29.4	792	7	CK777347
C 44	30.4	29.2	430	6	CA563031
C 45	30.4	29.2	446	2	BB840094

ALIGNMENTS

RESULT 1 BX118951 BX118951 474 bp mRNA linear EST 10-FEB-2003
LOCUS BX118951 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone
DEFINITION IMAGp998L124300 ; IMAGE:1693595, mRNA sequence.
ACCESSION BX118951
VERSION BX118951.1 GI:27882696
KEYWORDS EST.
SOURCE Homo sapiens (human) ;
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998L124300.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.

FEATURES

source

1. 474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998L124300 ; IMAGE:1693595"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NDHH19W"
/notes="Organ: heart; Vector: p773D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCATCTTTTTTTTTTTTTTTT 3'] ,

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

ORIGIN

Query Match 100.0%; Score 104; DB 5; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.7e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCTGACATCTG 60
|||||
Db 65 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCTGACATCTG 124
|||||
Qy 61 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGCGCAGAAATGCTGC 104
|||||
Db 125 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGCGCAGAAATGCTGC 168
|||||

RESULT 2

CB528492/c
LOCUS CB528492 630 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-Ft2-bjd-e-20-0-UI.s1 NCI CGAP_Ft2 Homo sapiens cDNA clone
UI-H-Ft2-bjd-e-20-0-UI 3', mRNA sequence.

ACCESSION CB528492
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 630)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 1-29, >AT_rich#Low_complexity (matched complement)
205-279, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
1..630
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-H-Ft2-bjd-e-20-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Ft2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ft2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library

construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-Ft2
TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCTGACATCTG 60
|||||
Db 503 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCTGACATCTG 444
|||||
Qy 61 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGCGCAGAAATGCTGC 104
|||||
Db 443 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGCGCAGAAATGCTGC 400
|||||

RESULT 3

CD370363/c
LOCUS CD370363 645 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-Ft1-bkb-n-03-0-UI.s1 NCI CGAP_Ft1 Homo sapiens cDNA clone
UI-H-Ft1-bkb-n-03-0-UI 3', mRNA sequence.

ACCESSION CD370363
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
1..645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-H-Ft1-bkb-n-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Ft1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; Control 3 hours; Control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 645;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 592 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 533

Qy 61 GAATCTGAGACACGAGGACCTTTGGTCTTGCCAGAAATGCTGC 104
Db 532 GAATCTGAGACACGAGGACCTTTGGTCTTGCCAGAAATGCTGC 489

RESULT 4

CD367676/c
LOCUS
DEFINITION
UI-H-FTI-bjr-1-14-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
UI-H-FTI-bjr-1-14-0-UI 3', mRNA sequence.
ACCESSION
CD367676.1 GI:31151766
VERSION
CD367676.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 688)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA

sequence: 69-143, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLVA=Yes.

FEATURES
source

Location/Qualifiers

1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bjr-1-14-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; Control 3 hours; Control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 367 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 308

Qy 61 GAATCTGAGACACGAGGACCTTTGGTCTTGCCAGAAATGCTGC 104
Db 307 GAATCTGAGACACGAGGACCTTTGGTCTTGCCAGAAATGCTGC 264

RESULT 5

CA307225/c
LOCUS
DEFINITION
UI-H-FTI-bhu-n-04-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
UI-H-FTI-bhu-n-04-0-UI 3', mRNA sequence.
ACCESSION
CA307225
VERSION
CA307225.1 GI:24470279
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 696)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..696
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-n-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(d1718 tail. The sequence tag for this library is
GGCCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT1
TAG_SEQ=GGCCATGCGG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAGTGGGGCTCCAGAACTCACTGGGCTACAGTTTGATCCCTGACATCTG 60
Db 594 GAATTCAGTGGGGCTCCAGAACTCACTGGGCTACAGTTTGATCCCTGACATCTG 535

Qy 61 GAATCTGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

Db 534 GAATCTGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 491

RESULT 6
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD364761 699 bp mRNA linear EST 05-AUG-2004
UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
CD364761
EST.
CD364761.1 GI:31148851
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 699)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..699
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjm-j-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtracted according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University
of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGG"

Query Match 100.0%; Score 104; DB 6; Length 699;

ORIGIN

Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 594 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 535
|||||
QY 61 GAATCTGGAGACAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
|||||
Db 534 GAATCTGGAGACAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 491
|||||

RESULT 7

CD368142/c

LOCUS

DEFINITION

UI-H-Ftl-bjv-e-20-0-UI.s1 NCI CGAP Ftl Homo sapiens cDNA clone

UI-H-Ftl-bjv-e-20-0-UI 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 298-372, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..703

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-Ftl-bjv-e-20-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stages="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Ftl"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site: 1: EcoR I; Site 2: Not I;

NCI CGAP Ftl is a normalized cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The mRNA samples

were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of

the conditions, other donor macrophages in different

conditions). The mRNA samples were pooled for library

construction. Control 0 hours; control 3 hours; control 24

hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;

PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella

moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus

moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral

vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector

(Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500,

3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS

3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3

hours; wt adenovirus + LPS 24 hours. The library was

normalized according to Bonaldo, Lennon and Soares, Genome

Research, 6:791-806, 1996. First strand cDNA synthesis was

primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-Ftl

TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match

Best Local Similarity 100.0%;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1

GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

|||||

Db 596

GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 537

|||||

QY 61

GAATCTGAGACAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104

|||||

Db 536

GAATCTGAGACAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 493

|||||

RESULT 8

CA308256/c

LOCUS

DEFINITION

UI-H-Ftl-bhy-e-14-0-UI.s1 NCI CGAP Ftl Homo sapiens cDNA clone

UI-H-Ftl-bhy-e-14-0-UI 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 296-370, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..713

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-Ftl-bhy-e-14-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stages="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Ftl"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site: 1: EcoR I; Site 2: Not I;

NCI CGAP Ftl is a normalized cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The mRNA samples

were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; Ad vector + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p77T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCGC. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 60
|||||
Db 594 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 535

Qy 61 GAATCTGAGACCGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 104
|||||
Db 534 GAATCTGAGACCGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 491

RESULT 9
CB528694/c
LOCUS
DEFINITION
UI-H-FT2-bjd-1-22-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.

ACCESSION
CB528694
VERSION
CB528694.1 GI:29388630
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 294-369, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
Location/Qualifiers
1..719
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-H-FT2-bjd-1-22-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_FT2"
/notes="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 60
|||||
Db 592 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 533

Qy 61 GAATCTGAGACCGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 104
|||||
Db 532 GAATCTGAGACCGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 489

RESULT 10
BQ007008/c
LOCUS
DEFINITION
UI-H-E11-azb-j-22-0-UI.s1 NCI CGAP_E11 Homo sapiens cDNA clone
IMAGE:5846517 3', mRNA sequence.

ACCESSION
BQ007008
VERSION
BQ007008.1 GI:19731908
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA
 sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..722
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5846517"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP E11"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACCTGGCAC.
 TAG_TISSUE=chondrosarcoma
 TAG_LIB=UI-H-E11
 TAG_SEQ=ACACTGCGAC"

ORIGIN

Query Match 100.0%; Score 104; DB 5; Length 722;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
 Db 595 GAATTTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536
 QY 61 GAATCTGGAGACACGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
 Db 535 GAATCTGGAGACACGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 492

RESULT 11
 CA307062/c
 LOCUS 722 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-F11-bhu-o-04-0-UI.s1 NCI CGAP_F11 Homo sapiens cDNA clone
 UI-H-F11-bhu-o-04-0-UI 3', mRNA sequence.
 ACCESSION CA307062
 VERSION CA307062.1 GI:24470116
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 722)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA
 sequence: 295-369, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..722
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-F11-bhu-o-04-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP F11"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP F11 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCGC. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-F11
 TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 722;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
 Db 593 GAATTTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 534
 QY 61 GAATCTGGAGACACGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
 Db 533 GAATCTGGAGACACGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 490

RESULT 12
 CD364988/c
 LOCUS 722 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-F12-bjn-c-04-0-UI.s1 NCI CGAP_F12 Homo sapiens cDNA clone
 UI-H-F12-bjn-c-04-0-UI 3', mRNA sequence.
 ACCESSION CD364988
 VERSION CD364988.1 GI:31149078
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)

REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-c-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGAACCTGGGGCCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 60
|||||
Db 595 GAATTCGAACCTGGGGCCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 536
|||||
QY 61 GAATCTGGAGACAGGGAGCCTTTGTTCTGTGCCAGAAATGCTGC 104
|||||
Db 535 GAATCTGGAGACAGGGAGCCTTTGTTCTGTGCCAGAAATGCTGC 492
|||||

RESULT 13
CA30877/c

LOCUS
DEFINITION

CA308777
UI-H-FT1-bhy-b-23-0-UI.s1 NCI CGAP_FTL Homo sapiens cDNA Clone
UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA308777.1 GI:24471831
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 723)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

RESULT 14	
CD368116/c	
LOCUS	723 bp mRNA linear EST 05-AUG-2004
DEFINITION	UI-H-FTI-bjv-a-04-0-UI.s1 NCI_CGAP_FTL Homo sapiens cDNA clone
ACCESSION	UI-H-FTI-bjv-a-04-0-UI 3', mRNA sequence.
VERSION	CD368116
KEYWORDS	CD368116.1 GI:31152206
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherii; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 723)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 The following repetitive elements were found in this cDNA
 sequence: 297-371, >(TAAA)nSimple repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

```

FEATURES
source
Location/Qualifiers
1. .723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl-bjv-a-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="NH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ftl"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_Ftl is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP) moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP) moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome

```

Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is GSCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-PT1
TAG_SEQ=GGCCATGCCG

ORIGIN	1AG_SEQ=GGCCCAIGCCG
Query Match	100.0%; Score 104; DB 6; Length 723;
Best Local Similarity	100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTCAGCTTTGATCCCTGACATCTG 60
Db	595 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTCAGCTTTGATCCCTGACATCTG 536
Qy	61 GAATCTGGAGACAGGAGCCTTTGGTTCTGGCCAGATGCTGC 104
Db	535 GAATCTGGAGACAGGAGCCTTTGGTTCTGGCCAGATGCTGC 492

RESULT 15
CA309711/c
LOCUS
DEFINITION
UI-H-FrT1-bic-b-17-0-UI.s1 NCI CGAP FrT1 Homo sapiens cDNA clone
UI-H-FrT1-bic-b-17-0-UI 3', mRNA sequence.
CA309711
ACCESSION
VERSION
CA309711.1 GI:24472765
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.

```

FEATURES
source
Location/Qualifiers
1. .724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl-bic-b-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ftl"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI_CGAP_Ftl is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to

```

incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; Control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIIB=UI-H-FT1 TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	100.0%	Score 104	DB 6	Length 724
Best Local Similarity	100.0%	Pred. No. 2.9e-21		
Matches 104	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG	60	
Db	595			
Qy	61	GAATCTGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	104	
Db	535			
		GAATCTGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	492	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 13:14:57 ; Search time 424.49 Seconds
(without alignments)
400.888 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaactggggctcc.....ggttctggccagaatgtgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	787	US-09-032-297A-13	Sequence 13, Appl
2	104	100.0	787	US-09-229-151C-7	Sequence 7, Appl
3	104	100.0	1585	US-09-023-655-1329	Sequence 1329, Ap
4	104	100.0	1587	US-09-949-016-5156	Sequence 5156, Ap
5	104	100.0	1643	US-08-880-342-36	Sequence 36, Appl
6	104	100.0	1643	US-09-505-250-4	Sequence 4, Appl
7	104	100.0	2270	US-09-229-151C-13	Sequence 13, Appl
8	104	100.0	2570	US-09-229-151C-14	Sequence 14, Appl
9	104	100.0	3634	US-09-166-186-1	Sequence 1, Appl
10	104	100.0	3634	US-09-313-932-1	Sequence 1, Appl
11	104	100.0	3634	US-09-109-663-34	Sequence 34, Appl
12	104	100.0	6682	US-09-949-016-16988	Sequence 16988, A
13	104	100.0	10728	US-09-376-774-5	Sequence 5, Appl
C 14	32.6	31.3	2623	US-09-976-594-142	Sequence 142, App
C 15	29.2	28.1	601	US-09-949-016-182065	Sequence 182065,
C 16	29.2	28.1	31713	US-09-949-016-16960	Sequence 16960, A
C 17	29	27.9	7517	US-09-949-016-15603	Sequence 15603, A
C 18	28.4	27.3	19601	US-09-949-016-15629	Sequence 15629, A
C 19	28	26.9	28720	US-09-341-587-7	Sequence 7, Appl
C 20	28	26.9	40905	US-09-949-016-16864	Sequence 16864, A
C 21	27.8	26.7	82125	US-09-949-016-13517	Sequence 13517, A
C 22	27.8	26.7	82125	US-09-949-016-13518	Sequence 13518, A
C 23	27.4	26.3	601	US-09-949-016-165185	Sequence 165185, A
C 24	27.4	26.3	102304	US-09-949-016-12589	Sequence 12589, A
C 25	27.4	26.3	116592	US-09-818-512-3	Sequence 3, Appl
C 26	27.4	26.3	124264	US-09-949-016-16396	Sequence 16396, A
C 27	27.2	26.2	412	US-09-621-976-19072	Sequence 19072, A

C 28	27.2	26.2	601	4	US-09-949-016-127063	Sequence 127063,
C 29	27.2	26.2	67479	4	US-09-949-016-11804	Sequence 11804, A
C 30	27.2	26.2	71119	4	US-09-949-016-15358	Sequence 15358, A
C 31	27	26.0	2903	4	US-09-949-016-5033	Sequence 5033, Ap
C 32	27	26.0	12695	4	US-09-949-016-16775	Sequence 16775, A
C 33	27	26.0	784019	4	US-09-949-016-14033	Sequence 14033, A
C 34	27	26.0	828152	4	US-09-949-016-12777	Sequence 12777, A
C 35	26.8	25.8	246444	4	US-09-949-016-13113	Sequence 13113, A
C 36	26.6	25.6	22287	4	US-09-949-016-16820	Sequence 16820, A
C 37	26.6	25.6	767677	4	US-09-949-016-12147	Sequence 12147, A
C 38	26.6	25.6	767677	4	US-09-949-016-17361	Sequence 17361, A
C 39	26.4	25.4	188	4	US-09-270-767-29222	Sequence 29222, A
C 40	26.4	25.4	868	4	US-09-270-767-13287	Sequence 13287, A
C 41	26.4	25.4	3170	4	US-09-169-768-1	Sequence 1, Appl
C 42	26.4	25.4	3171	4	US-09-169-768-15	Sequence 15, Appl
C 43	26.4	25.4	3181	1	US-08-655-086-1	Sequence 1, Appl
C 44	26.4	25.4	3349	4	US-09-169-768-13	Sequence 13, Appl
C 45	26.4	25.4	3531	4	US-09-169-768-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boehringer Ingelheim Corporation
; STREET: 900 Ridgebury Road, P.O. Box 368
; CITY: Ridgefield
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06877-0368
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,297A
; FILING DATE: 27-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,266
; FILING DATE: 28-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert P. Raymond
; REGISTRATION NUMBER: 25089
; REFERENCE/DOCKET NUMBER: 9/121PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-791-6183
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: DNA
; FEATURE:
; NAME/KEY: TNFa 3' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13
Query Match 100.0%; Score 104; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.2e-27;

```
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 60
Db |||||
222 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 281
Qy 61 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db |||||
282 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 325

RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 2.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

Query Match 100.0%; Score 104; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 60
Db 222 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGTTTGATCCCTGACATCTG 281
Qy 61 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 282 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 325

RESULT 3
US-09-023-655-1329
; Sequence 1329, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
```

```
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
US-09-023-655-1329

Query Match 100.0%; Score 104; DB 4; Length 1585;
Best Local Similarity 100.0%; Pred. No. 5.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062
Qy 61 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 1063 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 4
US-09-949-016-5156
; Sequence 5156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5156
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5156

Query Match 100.0%; Score 104; DB 4; Length 1587;
Best Local Similarity 100.0%; Pred. No. 5.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db 1005 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1064
Qy 61 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 1065 GAATCTGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1108
```

RESULT 5
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TNF CDNA HSTNFR (EMBL Accession
; INDIVIDUAL ISOLATE: #X01394)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..851
; US-08-880-342-36

Query Match 100.0%; Score 104; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 5.5e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129
QY 61 GAATCTGGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 6
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505.250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (153)...(854)
; US-09-505-250-4

Query Match 100.0%; Score 104; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 5.5e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129
QY 61 GAATCTGGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 7
US-09-229-151C-13
; Sequence 13, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229.151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 2.0
; SEQ ID NO 13
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
; US-09-229-151C-13

Query Match 100.0%; Score 104; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 6.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
DB 1705 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1764
QY 61 GAATCTGGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1765 GAATCTGGAGACACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1808

```
RESULT 8
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229.151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
US-09-229-151C-14

Query Match          100.0%; Score 104; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 6.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 2005 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGGCTACAGCTTTGATCCCTGACATCTG 2064
Qy 61 GAATCTGAGACACAGGAGCCTTTGGTCTTGCCCAAGATGCTGC 104
Db 2065 GAATCTGAGACACAGGAGCCTTTGGTCTTGCCCAAGATGCTGC 2108

RESULT 9
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166.186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
```

```
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; TITLE: homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match          100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 2808 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGGCTACAGCTTTGATCCCTGACATCTG 2867
Qy 61 GAATCTGGAGACACAGGAGCCTTTGGTCTTGCCCAAGATGCTGC 104
Db 2868 GAATCTGGAGACACAGGAGCCTTTGGTCTTGCCCAAGATGCTGC 2911

RESULT 10
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313.932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
```



```
/ LOCATION: (1635) .. (1821)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (1822) .. (1869)
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1870) .. (2070)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (2171) .. (3381)
/ PUBLICATION INFORMATION:
/ AUTHORS: Nedwin, G.E.
/ AUTHORS: Naylor, S.L.
/ AUTHORS: Sakaguchi, A.Y.
/ AUTHORS: Smith, D.
/ AUTHORS: Jarrett-Nedwin, J.
/ AUTHORS: Pennica, D.
/ AUTHORS: Goeddel, D.V.
/ TITLE: Human lymphotoxin and tumor necrosis factor genes:
/ TITLE: structure, homology and chromosomal localization
/ JOURNAL: Nucleic Acids Res.
/ VOLUME: 13
/ ISSUE: 17
/ PAGES: 6361-6373
/ DATE: 1985-09-11
/ DATABASE ACCESSION NUMBER: X02910 Genbank
/ DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db 2808 GAAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
Db 2868 GAAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 2911

RESULT 11
US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-301
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

Query Match 100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db 2808 GAAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60

QY 61 GAAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
Db 2868 GAAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 2911

RESULT 12
US-09-949-016-16898
; Sequence 16898, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16898
; LENGTH: 6682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16898

Query Match 100.0%; Score 104; DB 4; Length 6682;
Best Local Similarity 100.0%; Pred. No. 9e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
Db 4099 GAAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 4158

QY 61 GAAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
Db 4159 GAAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 4202

RESULT 13
US-09-376-774-5/c
; Sequence 5, Application US/09376774
; Patent No. 6759236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Gomer, Charles
; APPLICANT: T'Ang, Anne
; TITLE OF INVENTION: Methods To Enhance And Confine Expression
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT APPLICATION NUMBER: US/09/376,774
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 10728
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: recombinant vector pPATH-TNF?
US-09-376-774-5

Query Match 100.0%; Score 104; DB 4; Length 10728;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GAATTCAGAGCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTTGATCCCTGACATCTG 60
Db 4220 GAATTCAGAGCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTTGATCCCTGACATCTG 4161
QY 61 GAATCTGGAGACAGGAGGACCTTTGGTTCTTGCCAGAAATGCTGC 104
Db 4160 GAATCTGGAGACAGGAGGACCTTTGGTTCTTGCCAGAAATGCTGC 4117

RESULT 14
US-09-976-594-142/c
; Sequence 142, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 142
; LENGTH: 2623
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 337187.1
; NAME/KEY: unsure
; LOCATION: 2612
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-142

Query Match 31.3%; Score 32.6; DB 4; Length 2623;
Best Local Similarity 58.9%; Pred. No. 0.14;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 9 ACTGGGGCTCAGAACTCACTGGGGCTACAGCTTTTGATCCCTGACATCTGGAATCTGG 68
Db 359 ACTGGTCTGAGGTAGTAGCGGGGCTGTGCTGCTCCCTCCCGCTTGAGGGGG 300
QY 69 AGACCAGGAGCTTTGGTTCTTGCCAGAAATGCTG 103
Db 299 AGCCCTGAGGGCTCTGGGGCTGGGCTGGAAGGTG 265

RESULT 15
US-09-949-016-182065
; Sequence 182065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182065
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-182065

Query Match 28.1%; Score 29.2; DB 4; Length 601;
Best Local Similarity 65.2%; Pred. No. 1.4;
Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 6 CAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTTGATCCCTGACATCTGGAATC 65
Db 355 CAGACTGTGCCACCGCAGAGCTCCCTGGGGGCTTTTCTTTACCTCAGATATTTTGAAC 414
QY 66 TGGAGA 71
Db 415 TGAAGA 420

Search completed: September 2, 2005, 18:55:18
Job time : 428.49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 15:27:57 ; Search time 478.966 Seconds
(without alignments)
1421.994 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggcctcc.....ggtctggccagaatgctgc 104

Scoring table:

IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 733684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	104	9	US-09-801-371A-1
2	104	100.0	104	9	US-09-801-371A-5
3	104	100.0	787	18	US-10-356-308A-13
4	104	100.0	798	21	US-10-895-393-9
5	104	100.0	806	20	US-10-814-634A-5
6	104	100.0	1585	17	US-10-172-118-501
7	104	100.0	1585	18	US-10-342-887-501

8	104	100.0	1585	18	US-10-641-643-1329	Sequence 1329, Ap
9	104	100.0	1585	20	US-10-370-715B-19	Sequence 19, Appl
10	104	100.0	1643	15	US-10-272-411-4	Sequence 4, Appl
11	104	100.0	1643	15	US-10-218-547-3	Sequence 3, Appl
12	104	100.0	1643	15	US-10-272-328A-4	Sequence 4, Appl
13	104	100.0	1643	16	US-10-310-793-9	Sequence 9, Appl
14	104	100.0	1643	17	US-10-172-118-1901	Sequence 1901, Ap
15	104	100.0	1643	18	US-10-342-887-1901	Sequence 1901, Ap
16	104	100.0	1643	20	US-10-475-024-6	Sequence 6, Appl
17	104	100.0	1643	21	US-10-929-182-1	Sequence 1, Appl
18	104	100.0	1643	22	US-10-475-026-6	Sequence 6, Appl
19	104	100.0	1666	16	US-10-247-671-68	Sequence 68, Appl
20	104	100.0	1669	20	US-10-799-345-17	Sequence 17, Appl
21	104	100.0	1669	20	US-10-688-845-74	Sequence 74, Appl
22	104	100.0	2088	9	US-09-973-850-1	Sequence 1, Appl
23	104	100.0	2088	9	US-09-973-850-2	Sequence 2, Appl
24	104	100.0	2088	9	US-09-973-850-3	Sequence 3, Appl
25	104	100.0	3634	10	US-09-824-322B-1	Sequence 1, Appl
26	104	100.0	3634	10	US-09-932-300-34	Sequence 34, Appl
27	104	100.0	3634	17	US-10-191-997-104	Sequence 104, App
28	104	100.0	3634	18	US-10-202-062-3	Sequence 3, Appl
29	104	100.0	3634	19	US-10-652-795-1	Sequence 1, Appl
30	104	100.0	3634	19	US-10-647-918-1	Sequence 1, Appl
31	104	100.0	3634	21	US-10-770-970-1	Sequence 1, Appl
32	104	100.0	3634	24	US-11-028-780-3	Sequence 3, Appl
33	104	100.0	4830	17	US-10-429-802-33	Sequence 33, Appl
34	104	100.0	4830	17	US-10-430-503-24	Sequence 24, Appl
35	104	100.0	14036	21	US-10-741-600-17806	Sequence 17806, A
36	104	100.0	14769	21	US-10-741-600-18012	Sequence 18012, A
c 37	104	100.0	22173	19	US-10-322-696-28	Sequence 28, Appl
38	93	89.4	1279	16	US-10-247-671-120	Sequence 120, App
39	77	74.0	81	9	US-09-801-371A-7	Sequence 7, Appl
40	59.8	57.5	3673778	16	US-10-312-841-1	Sequence 1, Appl
41	58.2	56.0	3673778	16	US-10-312-841-2	Sequence 2, Appl
42	50	48.1	50	9	US-09-801-371A-8	Sequence 8, Appl
43	43	41.3	43	9	US-09-801-371A-2	Sequence 2, Appl
c 44	43	41.3	43	9	US-09-801-371A-6	Sequence 6, Appl
45	42	40.4	418	9	US-09-796-692-6223	Sequence 6223, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801.371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAACTGGGGCCTCCAGAACTCAGTGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||

Db 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 104
Db 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 104

RESULT 2

US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5
Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 104 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 45
Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 104
Db 44 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 1

RESULT 3

US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,266
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 1 to 787
; OTHER INFORMATION: TNFA 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13

; PAGES: 6361-6373
; DATE: 1985
US-10-356-308A-13
Query Match 100.0%; Score 104; DB 18; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 222 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281
Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 104
Db 282 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 325

RESULT 4

US-10-895-393-9
; Sequence 9, Application US/10895393
; Publication No. US20050048549A1
; GENERAL INFORMATION:
; APPLICANT: CAO, Liangxian
; APPLICANT: MEHTA, Anuradha
; APPLICANT: NARYSHKIN, Nikolai A.
; APPLICANT: PELLEGRINI, Matthew C.
; APPLICANT: ROMFO, Charles M.
; APPLICANT: TRIFILLIS, Panayiota
; APPLICANT: TROTTA, Christopher R.
; TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulat
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 19025.012
; CURRENT APPLICATION NUMBER: US/10/895,393
; CURRENT FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: PCT/US04/01643
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,637
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-895-393-9
Query Match 100.0%; Score 104; DB 21; Length 798;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 216 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 275
Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 104
Db 276 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCCGAAGATGCTGC 319

RESULT 5

US-10-814-634A-5
; Sequence 5, Application US/10814634A
; Publication No. US20040231007A1
; GENERAL INFORMATION:
; APPLICANT: CHENEVAL, Dominique
; APPLICANT: KASTELIC, Tania
; APPLICANT: Novation Pharmaceuticals Inc.
; TITLE OF INVENTION: Assay for Identifying Compounds Which
; TITLE OF INVENTION: Affect Stability of mRNA
; FILE REFERENCE: 793-104CIP
; CURRENT APPLICATION NUMBER: US/10/814,634A

```
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 09/869,159
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: GB 9828709.7
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-814-634A-5

Query Match      100.0%; Score 104; DB 20; Length 806;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 227 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 286

QY 61 GAATCTGGAGACAGGAGCCTTTGGTCTGCGCCAGAAATGCTGC 104
Db 287 GAATCTGGAGACAGGAGCCTTTGGTCTGCGCCAGAAATGCTGC 330

RESULT 6
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Bernards, Rene
; APPLICANT: Van de Vijver, Marc
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501

Query Match      100.0%; Score 104; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACAGGAGCCTTTGGTCTGCGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACAGGAGCCTTTGGTCTGCGCCAGAAATGCTGC 1106

RESULT 7
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-501

Query Match      100.0%; Score 104; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACAGGAGCCTTTGGTCTGCGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACAGGAGCCTTTGGTCTGCGCCAGAAATGCTGC 1106

RESULT 8
US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match      100.0%; Score 104; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 1106

RESULT 9
US-10-370-715B-19
; Sequence 19, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; RELATED DISEASES
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 19
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-19

Query Match      100.0%; Score 104; DB 20; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 1106

RESULT 10
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
```

```
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match      100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
Db 1130 GAATCTGGAGACAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 1173

RESULT 11
US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3

Query Match      100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
```

```
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
    61 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 104
    1130 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 1173

RESULT 12
US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US2003010944A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-4

Query Match 100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
    61 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 104
    1130 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 1173

RESULT 13
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
```

```
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-310-793-9

Query Match 100.0%; Score 104; DB 16; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
    61 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 104
    1130 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 1173

RESULT 14
US-10-172-118-1901
; Sequence 1901, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: X01394
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1901

Query Match 100.0%; Score 104; DB 17; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
    61 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 104
    1130 GAATCTGAGACACAGGAGCCTTTGGTTCTTGCCCGAGAATGCTGC 1173

RESULT 15
US-10-342-887-1901
; Sequence 1901, Application US/10342887
```

```
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1901

Query Match      100.0%; Score 104; DB 18; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||||||
Db      1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy      61  GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
      |||||||
Db      1130 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173
```

Search completed: September 3, 2005, 00:21:56
Job time : 484.966 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:55:28 ; Search time 783.946 Seconds
(without alignments)
2657.805 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43
Sequence: 1 tcaaaactgggctccagaa.....actgggctacagatttga 43

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_phi.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	400	11	GI3533
2	43	100.0	787	6	BD137681 Self-regu
3	43	100.0	787	6	AR300453 Sequence
4	43	100.0	787	6	BD070551 Self-regu
5	43	100.0	817	6	AI6444 Xho-PstI fr
6	43	100.0	817	6	E02109 DNA sequenc
7	43	100.0	1047	9	AJ249755 Homo sapi
8	43	100.0	1275	6	I08430 Sequence 5
9	43	100.0	1323	6	I07953 Sequence 6
10	43	100.0	1324	6	E00702 cDNA encodi
11	43	100.0	1324	6	I03610 Sequence 2
12	43	100.0	1379	12	M35592 Synthetic h
13	43	100.0	1465	6	I04244 Sequence 2
14	43	100.0	1560	6	I08863 Sequence 3
15	43	100.0	1585	6	A37272 Sequence 12
16	43	100.0	1585	6	I04169 Sequence 1
17	43	100.0	1585	6	I04198 Sequence 1
18	43	100.0	1585	6	I08384 Sequence 5
19	43	100.0	1585	6	I08429 Sequence 3

20	43	100.0	1585	6	AR380784	AR380784 Sequence
21	43	100.0	1585	9	HUMTNFAA	M10988 Human tumor
22	43	100.0	1606	6	I07541	I07541 Sequence 22
23	43	100.0	1643	6	AR146199	AR146199 Sequence
24	43	100.0	1643	6	AR366225	AR366225 Sequence
25	43	100.0	1643	9	HSTNFR	X01394 Human mRNA
26	43	100.0	1676	9	BC028148	BC028148 Homo sapi
27	43	100.0	2270	6	BD137687	BD137687 Self-regu
28	43	100.0	2270	6	AR300459	AR300459 Sequence
29	43	100.0	2570	6	BD137688	BD137688 Self-regu
30	43	100.0	2570	6	AR300460	AR300460 Sequence
31	43	100.0	3103	9	HUMTNFX	M26331 Human tumor
32	43	100.0	3634	6	AR100270	AR100270 Sequence
33	43	100.0	3634	6	AR149925	AR149925 Sequence
34	43	100.0	3634	6	BD227798	BD227798 Antisense
35	43	100.0	3634	6	BD271232	BD271232 Predictio
36	43	100.0	3634	6	BD064008	BD064008 Novel exp
37	43	100.0	3634	9	HSTNFA	X02910 Human gene
38	43	100.0	4830	9	AY066019	AY066019 Homo sapi
39	43	100.0	6974	9	AB088112	AB088112 Homo sapi
40	43	100.0	7112	6	AX100950	AX100950 Sequence
41	43	100.0	7112	6	AX100965	AX100965 Sequence
42	43	100.0	7112	9	HUMTNFAB	M16441 Human tumor
43	43	100.0	7240	9	AY214167	AY214167 Homo sapi
C 44	43	100.0	10728	6	AR562497	AR562497 Sequence
C 45	43	100.0	16310	9	HSTNFABX	Z15026 Homo sapien

ALIGNMENTS

RESULT 1

GI3533

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

GI3533 SHGC-11076 Human Homo sapiens STS genomic, linear STS 30-MAR-2000

GI3533 SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.

GI3533.1 GI:1129272

STS.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)

Olivier, M. and Cox, D.R.

Unpublished, Olivier, M., Cox, D.R. (2000)

Unpublished (2000)

Contact: Michael Olivier, David R. Cox

Stanford Human Genome Center

Stanford University School of Medicine

4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA

Tel: (650) 320-5800

Fax: (650) 320-5801

Email: olivier@shgc.stanford.edu

Primer A: CACTAAGATTCAACTGGGC

Primer B: GAGGAGGCTTAAGTCCAC

STS size: 166

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2:	2.5 mM																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
--------	--------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

```

RESULT 5
LOCUS      Al6444
DEFINITION Xho-PstI fragment from THP-I cells.
ACCESSION  Al6444
VERSION     Al6444.1 GI:641014
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 817)
AUTHORS     Soma,G.I., Mizuno,D., Tsuji,Y. and Kobayashi,N.
TITLE       Anti-aids preparation
JOURNAL     Patent: EP 0450240-A 9 09-OCT-1991;
            Soma, Gen-Ichiro; Mizuno, Den'ichi
FEATURES   Location/Qualifiers
            source
            1..817
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 43; DB 6; Length 817;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
Db      716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 758

RESULT 6
LOCUS      E02109
DEFINITION DNA sequence coding for anti-tumor polypeptide.
ACCESSION  E02109
VERSION     E02109.1 GI:2170351
KEYWORDS   JP 1989256390-A/1.
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 817)
AUTHORS     Soma,G., Mizuno,D. and Tsuji,Y.
TITLE       NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL
            POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT
            FROM SAID POLYPEPTIDE
JOURNAL     Patent: JP 1989256390-A 1 12-OCT-1989;
            SOMA GENICHIRO, MIZUNO DENICHI
COMMENT     PN JP 1989256390-A/1
            PD 12-OCT-1989
            PF 03-APR-1988 JP 1988081683
            PI SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIAKI PC
            C12N15/00,A61K37/24,C07K13/00,C12P21/02,(C12P21/02,C12R1:19); CC
            strandedness: Double;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: No;
            CC *source: library=THP-1 cell;
            FH Key Location/Qualifiers
            FT mat_peptide >1..<817
            FT /product='Anti-tumor polypeptide'.
FEATURES   Location/Qualifiers
            source
            1..817
            /organism="Glycine max"
            /mol_type="genomic DNA"
            /db_xref="taxon:3847"
ORIGIN

```

```

Query Match      100.0%; Score 43; DB 6; Length 817;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
Db      716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 758

RESULT 7
LOCUS      HSA249755
DEFINITION Homo sapiens TNF-alpha gene for tumor necrosis factor-alpha, 3'
            UTR, country United Arab Emirates.
ACCESSION  AJ249755
VERSION     AJ249755.1 GI:6002308
KEYWORDS   TNF-alpha gene; tumor necrosis factor-alpha.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Farhan,A.J., Pravica,V. and Hutchinson,I.V.
TITLE       Identification of new rare variant of human TNF-alpha 3' UTR
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1047)
AUTHORS     Farhan,A.J.
TITLE       Direct Submission
JOURNAL     Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research
            Division, Manchester University, Medical School, Stopford Building,
            Oxford Road, Manchester, M13 9PT, UNITED KINGDOM
FEATURES   Location/Qualifiers
            source
            1..1047
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /country="United Arab Emirates"
            /note="new rare variant"
            gene
            1..1047
            /gene="TNF-alpha"
            3'UTR
            1..>1047
            /gene="TNF-alpha"
            variation
            322
            /gene="TNF-alpha"
            /replace="t"
ORIGIN
Query Match      100.0%; Score 43; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
Db      225 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 267

RESULT 8
LOCUS      I08430
DEFINITION Sequence 5 from Patent WO 8604606.
ACCESSION  I08430
VERSION     I08430.1 GI:588860
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1275)
AUTHORS     Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE       CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
            NECROSIS FACTOR PROTEINS
JOURNAL     Patent: WO 8604606-A 5 14-AUG-1986;
            Location/Qualifiers
FEATURES   source
            1..1275

```


JOURNAL Nucleic Acids Symp. Ser. 17, 131-134 (1986)
MEDLINE 87174864
PUBMED 3031624
COMMENT Original source text: Altered human leukemic B-cell line Ball-1,
CDNA to mRNA, clone pM324-346.
FEATURES
source Location/Qualifiers
1..1379
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
CDS 178..879
/note="synthetic tumor necrosis factor precursor"
/codon_start=1
/transl_table=1
/protein_id="AAC42098.1"
/db_xref="GI:209486"
/translation="MSTSMIRDVELAEALPKYGGPGQSRRCFLFLSFLIVAGA
TTLFLLHFGVMGQREFFPRDLISPLAQVRSSTPSDKPVAVHVVANPQAGQL
QWLNRRANALLANGVELRDNLVVPSEGLYLIYQVLPKGGQCPSTHLLTHTISRIA
VSYQTKVNLLSAISKPCQRETPEGAEPWYPIYLGGVFQLEKGRLSAEINRPDYL
DPAESGVYFGIALL"
sig_peptide 178..399
/note="synthetic tumor necrosis factor signal peptide"
mat_peptide 400..876
/product="synthetic tumor necrosis factor"
ORIGIN
Query Match 100.0%; Score 43; DB 12; Length 1379;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 1100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 1142
RESULT 13
LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION I04244
VERSION I04244.1 GI:268725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Lin, L.S. and Yamamoto, R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source Location/Qualifiers
1..1465
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 887 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 929
RESULT 14
LOCUS I08863 1560 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8806625.
ACCESSION I08863
VERSION I08863.1 GI:588416
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Mark, D.F., Lin, L.S., Thomason, J.W. and Yamamoto, R.
TITLE ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8806625-A 3 07-SEP-1988;
FEATURES Location/Qualifiers
source 1..1560
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 1049
RESULT 15
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.
ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1585)
AUTHORS Vile, R.G. and Hart, I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
FEATURES Location/Qualifiers
source 1..1585
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 1049
Search completed: September 3, 2005, 01:14:21
Job time : 784.946 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:45:43 ; Search time 131.925 Seconds
(without alignments)
1929.494 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaactggggccctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980a:*
2: Geneseqn1990a:*
3: Geneseqn2000a:*
4: Geneseqn2001a:*
5: Geneseqn2001bs:*
6: Geneseqn2002a:*
7: Geneseqn2002bs:*
8: Geneseqn2003a:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004a:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	43	AAZ99817	AAZ99817 Cis-actin
2	43	100.0	50	AAZ99815	AAZ99815 Sequence
3	43	100.0	104	AAZ99816	AAZ99816 Cis-actin
4	43	100.0	787	AAZ20979	AAZ20979 Human TNF
5	43	100.0	792	ADR12297	ADR12297 Human tum
6	43	100.0	815	1AAN70075	1AAN70075 Human ant
7	43	100.0	817	2AAQ04340	2AAQ04340 THP-1. 3/
8	43	100.0	818	1AAN91035	1AAN91035 XhoI - Ps
9	43	100.0	1200	1AAN70072	1AAN70072 Human ant
10	43	100.0	1200	1AAN90969	1AAN90969 Part of g
11	43	100.0	1275	1AAN60558	1AAN60558 Sequence
12	43	100.0	1279	10ADE25716	10ADE25716 Human cdn
13	43	100.0	1323	1AAN60363	1AAN60363 Sequence
14	43	100.0	1324	3AA34963	3AA34963 Human ade
15	43	100.0	1324	3AAF21085	3AAF21085 Human low
16	43	100.0	1324	10ABZ96779	10ABZ96779 Human nuc
17	43	100.0	1324	11ABD20628	11ABD20628 Human pul
18	43	100.0	1560	1AAN80219	1AAN80219 Sequence
19	43	100.0	1581	12ADQ83817	12ADQ83817 Human tum
20	43	100.0	1585	1AAN60527	1AAN60527 Sequence

21	43	100.0	1585	1AAN60557	1AAN60557 Sequence
22	43	100.0	1585	8ACA64836	8ACA64836 Human TNF
23	43	100.0	1585	10ADF76346	10ADF76346 Novel hum
24	43	100.0	1585	11ADI32003	11ADI32003 Human cdn
25	43	100.0	1585	12ADO19587	12ADO19587 Human PRO
26	43	100.0	1585	13ADR24640	13ADR24640 Breast ca
27	43	100.0	1585	13ADP54654	13ADP54654 Human PRO
28	43	100.0	1606	1AAN60446	1AAN60446 Sequence
29	43	100.0	1606	2AAT15424	2AAT15424 Human tum
30	43	100.0	1643	1AAN71307	1AAN71307 Sequence
31	43	100.0	1643	2AAT31021	2AAT31021 Human tum
32	43	100.0	1643	8ABK13195	8ABK13195 Human tum
33	43	100.0	1643	6AAL53712	6AAL53712 Tumour ne
34	43	100.0	1643	10AD49644	10AD49644 Human tum
35	43	100.0	1643	8ADC35185	8ADC35185 Human cdn
36	43	100.0	1643	10AAD63904	10AAD63904 Human TNF
37	43	100.0	1643	10ACC57575	10ACC57575 Polynucle
38	43	100.0	1643	13ADR26040	13ADR26040 Breast ca
39	43	100.0	1650	8ACF64375	8ACF64375 Human TNF
40	43	100.0	1666	10ADE25664	10ADE25664 Human cdn
41	43	100.0	1669	13ADS88038	13ADS88038 Tumour tr
42	43	100.0	1669	13ADT08160	13ADT08160 Human tum
43	43	100.0	2270	2AAZ20983	2AAZ20983 Chimeric
44	43	100.0	2570	2AAZ20984	2AAZ20984 Chimeric
45	43	100.0	3634	2AAV39005	2AAV39005 TNF-alpha

ALIGNMENTS

RESULT 1
AAZ99817
ID AAZ99817 standard; RNA; 43 BP.
XX
AC AAZ99817;
XX

DT 12-JUL-2000 (first entry)

XX Cis-acting nucleotide sequence derived from human TNF-alpha.

XX Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eif2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX

OS Homo sapiens.

XX WO200014255-A1.

XX PD 16-MAR-2000.

XX PF 06-SEP-1999; 99WO-IL0000483.

XX PR 07-SEP-1998; 98IL-00126112.

XX PR 26-OCT-1998; 98IL-00126757.

XX (YISS) YISSUM RES & DEV CO.

XX PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX WPI; 2000-257000/22.

XX Regulation of gene expression by mRNA splicing is carried out using a cis-acting nucleotide sequence controlled by phosphorylation of the alpha-subunit of eukaryotic initiation factor 2.

XX Claim 5; Page 15; 75pp; English.

XX The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic

Best Local Similarity 100.0%; Pred. No. 5e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
DB 5 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 47

RESULT 4

AAZ20979
ID AAZ20979 standard; DNA; 787 BP.

XX AAZ20979;

XX 30-NOV-1999 (first entry)

XX Human TNFalpha 3'UTR.

XX TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
KW ankylosing spondylitis; rheumatoid arthritis; ds.

XX Homo sapiens.

XX WO9943840-A1.

XX 02-SEP-1999.

XX 12-JAN-1999; 99WO-US000637.

XX 27-FEB-1998; 98US-0076316P.

XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX Tataka RJ, Marlin SD, Barton RW;

XX WPI; 1999-527630/44.

XX A chimeric polynucleotide consisting of a tissue necrosis factor (TNF)
PT promoter and an apoptosis-inducing Granzyme B polynucleotide.

XX Example 1; Page 60-61; 71pp; English.

XX This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
CC constructed comprising at least one TNFalpha promoter enhancer region
CC (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA encoding
CC the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha
CC 3'UTR sequence. TNFalpha is one of a number of cytokines produced by
CC inflammatory cells. Upregulation and/or dysregulation of cytokines in
CC inflamed tissue may be directly or indirectly responsible for
CC exacerbation of chronic inflammatory diseases. Introduction of the
CC chimeric nucleotide to activated inflammatory cells causes them to
CC undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide
CC may be useful for treating inflammatory disorders such as multiple
CC sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus
CC host disease, lupus erythematosus, insulin-dependent (type II) diabetes
CC mellitus, ankylosing spondylitis, and in particular, rheumatoid
CC arthritis. The use of such chimeric nucleotides offers simpler and
CC cheaper long-term relief, in comparison with existing conventional
CC pharmaceutical and invasive surgery methods

SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
DB 226 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 268

RESULT 5

ADR12297

ID ADR12297 standard; DNA; 792 BP.

XX ADR12297;

XX 21-OCT-2004 (first entry)

XX Human tumour necrosis factor alpha 3'-untranslated region DNA.

XX as; cytostatic; VEGF modulator; angiogenesis inhibitor;
KW UTR-dependent expression; vascular endothelial growth factor;
KW untranslated region; cancer; angiogenesis.

XX Homo sapiens.

XX WO2004065561-A2.

XX 05-AUG-2004.

XX 21-JAN-2004; 2004WO-US001643.

XX 21-JAN-2003; 2003US-0441637P.

XX (PTCT-) PTC THERAPEUTICS INC.

XX Cao L, Trifillis P;

XX WPI; 2004-571681/55.

XX Identifying modulators of untranslated region-dependent expression of a
PT VEGF gene, useful for treating cancer, comprises contacting a compound
PT with a cell or translation mixture containing a reporter gene linked to a
PT VEGF gene UTR.

XX Example; SEQ ID NO 6; 251pp; English.

XX A method of identifying (M1) a compound that modulates untranslated
CC region-dependent expression of a vascular endothelial growth factor
CC (VEGF) gene comprises contacting a member of a library of compounds with
CC a cell or cell-free translation mixture containing a reporter gene
CC operably linked to an untranslated region (UTR) of the VEGF gene, and
CC detecting expression of the reporter gene. A compound is identified as
CC modulator if the level of expression of the reporter gene in the presence
CC of the compound is altered as compared to that in the absence of the
CC compound or in the presence of a control. Compounds identified by M1 are
CC useful for treating, preventing or ameliorating cancer or its symptoms,
CC and/or for inhibiting angiogenesis. This sequence corresponds to a
CC therapeutic untranslated region used in the invention.

SQ Sequence 792 BP; 192 A; 203 C; 172 G; 225 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 13; Length 792;

Best Local Similarity 100.0%; Pred. No. 6.8e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
DB 223 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 265

RESULT 6

AA70075

ID AA70075 standard; DNA; 815 BP.

XX AA70075;

XX 25-MAR-2003 (revised)

XX 20-JAN-1991 (first entry)

XX Human anti-tumor polypeptide Xho-PstI fragment.

KW Anti-tumor; cancer; cytotoxic; ss.
XX
OS Homo sapiens.
XX
XX EP247906-A.
PN
XX
XX PD 02-DEC-1987.
XX
XX PF 04-FEB-1987; 87EP-00400261.
XX
XX PR 04-FEB-1986; 86JP-00021302.
XX
XX PR 07-FEB-1986; 86JP-00024220.
XX
XX PR 17-JUL-1986; 86JP-00169522.
XX
XX PA (MIZU/) MIZUNO D.
XX
XX PI Mizuno D, Soma GI;
XX
XX WPI; 1987-336540/48.
XX
XX PT Anti-tumour polypeptide(s) - prep'd. using recombinant DNA prep'd. from
XX PT genomic DNA of human acute leukaemia cell thp-1.
XX
XX PS Disclosure; Fig 7; 63pp; English.
XX
XX CC The sequence is an Xho-PstI fragment of an anti-tumor protein. The
XX CC polypeptide is cytotoxic to human tumor cells but not to normal cells.
XX CC They are also cytotoxic to primary cell cultures obtained from metastasis
XX CC lesions of patients suffering from striated muscle tumors. They are also
XX CC resistant to all chemotherapeutic agents. See also AAN70073-74, AAP70077-
XX CC 78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 815;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758

RESULT 7
AAQ04340
ID AAQ04340 standard; DNA; 817 BP.
XX
XX AC AAQ04340;
XX
XX DT 25-MAR-2003 (revised)
XX DT 21-SEP-1990 (first entry)
XX
XX DE THP-1.
XX
XX KW Acute leukaemia cell; THP-1; anti-tumour agent; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP02088598-A.
XX
XX PD 28-MAR-1990.
XX
XX PF 22-SEP-1988; 86JP-00239154.
XX
XX PR 22-SEP-1988; 86JP-00239154.
XX
XX PA (SOMA/) SOMA G.
XX
XX DR WPI; 1990-143138/19.
XX
XX PT Intrinsic TNF prodn. derivation agents - contain primer and trigger, at
XX PT least one of which has TNF activity.
XX

PS Disclosure; Page ?; 26pp; Japanese.
XX
XX CC Used in the prodn. of TNF prodn. agents. (Updated on 25-MAR-2003 to
XX CC correct PD field.)
XX
XX SQ Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758

RESULT 8
AAN91035
ID AAN91035 standard; DNA; 818 BP.
XX
XX AC AAN91035;
XX
XX DT 27-AUG-2003 (revised)
XX DT 11-MAR-1990 (first entry)
XX
XX DE XhoI - PstI section of gene for anti-cancer peptide.
XX
XX KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX
XX OS THP 1 cells.
XX
XX PN JP01095784-A.
XX
XX PD 13-APR-1989.
XX
XX PF 06-OCT-1987; 87JP-00252174.
XX
XX PR 06-OCT-1987; 87JP-00252174.
XX
XX PA (SENG/) SEN G.
XX
XX DR WPI; 1989-154899/21.
XX
XX PT Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic
XX PT agents.
XX
XX PS Fig 3; Page ?; 17pp; Japanese.
XX
XX CC Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA
XX CC from THP-1 cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 818;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 717 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 759

RESULT 9
AAN70072
ID AAN70072 standard; DNA; 1200 BP.
XX
XX AC AAN70072;
XX
XX DT 25-MAR-2003 (revised)
XX DT 20-JAN-1991 (first entry)
XX
XX DE Human anti-tumor polypeptide.
XX

KW Anti-tumor; cancer; cytotoxic; ss.
 XX Homo sapiens.
 XX EP247906-A.
 XX 02-DEC-1987.
 XX 04-FEB-1987; 87EP-00400261.
 XX 04-FEB-1986; 86JP-00021302.
 PR 07-FEB-1986; 86JP-00024220.
 PR 17-JUL-1986; 86JP-00169522.
 XX (MIZU/) MIZUNO D.
 XX Mizuno D, Soma GI;
 XX WPI; 1987-336540/48.
 XX Anti-tumor polypeptide(s) - prep'd. using recombinant DNA prep'd. from
 PT genomic DNA of human acute leukaemia cell thp-1.
 XX Disclosure; Fig 4; 63pp; English.
 XX The polypeptide is cytotoxic to human tumor cells but not to normal
 CC cells. They are also cytotoxic to primary cell cultures obtained from
 CC metastasis lesions of patients suffering from striated muscle tumors.
 CC They are also resistant to all chemotherapeutic agents. See also AAN70073
 CC -75; AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR
 CC field.)
 XX Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 43; DB 1; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 Db 1099 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1141
 RESULT 10
 AAN90969
 ID AAN90969 standard; DNA; 1200 BP.
 XX AC AAN90969;
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 11-MAR-1990 (first entry)
 XX Part of gene for anti-cancer peptide.
 DE Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
 KW THP 1 cells.
 OS JP01095784-A.
 XX 13-APR-1989.
 XX 06-OCT-1987; 87JP-00252174.
 XX 06-OCT-1987; 87JP-00252174.
 XX (SENG/) SEN G.
 XX WPI; 1989-154899/21.
 XX Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic
 PT agents.

XX Fig 2; Page 7; 17pp; Japanese.
 PS Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1
 CC cells. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-
 CC 2003 to correct OS field.)
 XX Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 43; DB 1; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 Db 1099 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1141
 RESULT 11
 AAN60558
 ID AAN60558 standard; DNA; 1275 BP.
 XX AC AAN60558;
 XX 28-JUL-1991 (first entry)
 DT Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
 DE 69 in pAW731.
 XX Antitumour; anticancer; ss.
 KW Homo sapiens.
 OS Key Location/Qualifiers
 XX CDS 1..474
 FT /*tag= a
 XX WO8604606-A.
 XX 14-AUG-1986.
 XX 03-FEB-1986; 86WO-US000236.
 XX 07-FEB-1985; 85US-00698939.
 XX (CETU) CETUS CORP.
 XX Mark DF, Lin LS, Lu SDY, Wang AM;
 PI WPI; 1986-225458/34.
 DR P-PSDB; AAP60656.
 XX New synthetic muteins of human tumour necrosis factor protein - are obt'd.
 PT by direct mutagenesis and retain antitumour activity.
 XX Disclosure; Fig 3a; 47pp; English.
 XX The sequence encoding TNF produced by the promyelocytic leukemia cell
 CC line (HL-60, ATCC no. CCL240) has been cloned and expressed in E.coli (see
 CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
 CC sequence appears to be involved in disulphide linkages. The patentors
 CC claim a novel synthetic mutein of a biologically active hTNF protein,
 CC having at least one cysteine residue free from a disulphide link and non-
 CC essential to the activity and having at least one of the cysteine
 CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
 CC claimed
 XX Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 43; DB 1; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 7.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db |||||||||||||||||||||||||||||||||||||||||||
697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739

RESULT 12
ADE25716
ID ADE25716 standard; cDNA; 1279 BP.
XX AC ADE25716;
XX DT 29-JAN-2004 (first entry)
XX DE Human cDNA differentially expressed in foam cells #120.
XX KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
XX KW cardiovascular disease; atherosclerosis.
XX OS Homo sapiens.
XX PN US2003194721-A1.
XX PD 16-OCT-2003.
XX PF 18-SEP-2002; 2002US-00247671.
XX PR 19-SEP-2001; 2001US-0323784P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Mikita T, Shiffman D, Porter JG, Kaser MR;
XX WPI; 2003-875398/81.
XX DR P-PSDB; ADE25778.
XX
XX Combination containing several polynucleotide that are differentially
XX expressed in foam cells and complements of the polynucleotides, useful
XX for diagnosing cardiovascular disease or atherosclerosis.
XX
XX Claim 1; SEQ ID NO 120; 37pp; English.
XX
XX The invention relates to a combination comprising several polynucleotides
XX having any one of 127 sequences (S1) such as the sequence of human
XX calmodulin gene, human mRNA for KIAA930 protein, leukotriene A4
XX hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
XX mRNA, etc., and their complements. The cDNAs are differentially expressed
XX in LPS (lipopolysaccharide)-treated foam cells. Also included are
XX obtaining an extended or full length gene from a library of nucleic acid
XX sequences, an expression vector containing the nucleic acids, a host cell
XX containing the vector, a purified polypeptide appearing as ADE25750 and
XX ADE25751, producing a protein by culturing the host cell, and a
XX composition comprising a purified antibody that specifically binds to the
XX proteins. The foam cell-expressed nucleic acids are useful for a high
XX throughput detection of differential expression of one or more
XX polynucleotides in a sample. The sample is from a subject with
XX atherosclerosis and comparison with a standard defines early, mid or late
XX stages of the disorder. The foam cell-expressed nucleic acids are useful
XX for high throughput screening of a library of molecules or compounds to
XX identify a ligand which binds a polynucleotide. The library is chosen
XX from DNA molecules, peptides, proteins and RNA molecules. The protein is
XX useful for a high throughput screening of library of molecules or
XX compounds to identify at least one ligand which specifically binds a
XX protein, for purifying a ligand from a sample for making an antibody. The
XX foam cell-expressed nucleic acids are useful for diagnosing
XX cardiovascular disorder. The foam cell-expressed nucleic acids are useful
XX as elements on a microarray which can be used for detecting related
XX polynucleotide in a sample, diagnosing cardiovascular disease,
XX atherosclerosis. The present sequence represents a cDNA whose expression
XX is upregulated in LPS treated foam cells.
XX
XX Sequence 1279 BP; 293 A; 415 C; 323 G; 248 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 43; DB 10; Length 1279;
Best Local Similarity 100.0%; Pred. No. 7 4e-07;
Matches 43; Conservative 0; Mismatches 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db |||||||||||||||||||||||||||||||||||||||||||
754 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 796

Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db |||||||||||||||||||||||||||||||||||||||||||
1081 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1123

RESULT 13
AAN60363
ID AAN60363 standard; DNA; 1323 BP.
XX AC AAN60363;
XX DT 19-JUN-1991 (first entry)
XX DE Sequence encoding human tumour necrosis factor.
XX KW hTNF; tumour; cancer; interferon; ds.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..534
XX FT sig_peptide 1..60
XX FT mat_peptide 61..534
XX FT sig_peptide /tag= a
XX FT mat_peptide /tag= b
XX FT mat_peptide /label= Secretory leader peptide
XX FT mat_peptide /tag= c
XX
XX EPI68214-A.
XX
XX 15-JAN-1986.
XX
XX 03-JUL-1985; 85EP-00304758.
XX
XX 05-JUL-1984; 84US-00627959.
XX 05-JUL-1984; 84US-00628059.
XX 05-JUL-1984; 84US-00628060.
XX 03-DEC-1984; 84US-00677156.
XX 03-DEC-1984; 84US-00677257.
XX 03-DEC-1984; 84US-00677267.
XX 03-DEC-1984; 84US-00677454.
XX
XX (GETH ) GENENTECH INC.
XX
XX Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;
XX WPI; 1986-015483/03.
XX P-PSDB; AAP60417.
XX
XX Pure tumour necrosis factor and mutant forms - new DNA coding sequences
XX and transformed cells.
XX
XX Claim 20; Fig 10; 90pp; English.
XX
XX Sequence encodes the pure human tumour necrosis factor, mutants of which
XX are covered by the claims. TNF and mutants are useful in treating
XX tumours, especially in tandem with interferon. The encoding sequence may
XX be used to create plasmid pTRXAPTf, allowing transformation of an
XX E.coli host for the expression of TNF
XX
XX Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 43; DB 1; Length 1323;
Best Local Similarity 100.0%; Pred. No. 7 4e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db |||||||||||||||||||||||||||||||||||||||||||
754 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 796
```

RESULT 14
 AAA34963
 ID AAA34963 standard; DNA; 1324 BP.
 XX
 AC AAA34963;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.
 XX
 KW Human: adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 WPI; 2000-205971/18.
 XX
 DR
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 814-815; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytotatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA3392) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 |||||
 DB 755 TCNAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 797
 RESULT 15
 AAF21085
 ID AAF21085 standard; DNA; 1324 BP.
 XX
 AC AAF21085;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2652.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytotatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI NYCE J W.
 XX
 WPI; 2000-679539/66.
 XX
 DR Low adenosine (A) content antisense oligonucleotides which do not trigger
 DR adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 PT
 PS Disclosure; Page 887; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytotatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,

CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 3; Length 1324;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

Db 755 TCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797

Search completed: September 3, 2005, 00:29:35

Job time : 132.925 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 23:36:03 ; Search time 983.15 Seconds
(without alignments)
1664.816 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43
Sequence: 1 tcaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	248	7	T29839 EST97164 Hu
2	43	100.0	474	5	BX118951
3	43	100.0	630	6	CB528492 UI-H-FT1
4	43	100.0	645	6	CB370363 UI-H-FT1
5	43	100.0	684	6	CA307429 UI-H-FT1
6	43	100.0	688	6	CB367676 UI-H-FT1
7	43	100.0	696	6	CA307225 UI-H-FT1
8	43	100.0	699	6	CD364761 UI-H-FT1
9	43	100.0	703	6	CD368142 UI-H-FT1
10	43	100.0	713	6	CA308256 UI-H-FT1
11	43	100.0	719	6	CB528694 UI-H-FT1
12	43	100.0	722	5	BQ007008 UI-H-E11
13	43	100.0	722	6	CA307062 UI-H-FT1
14	43	100.0	722	6	CD364988 UI-H-FT1
15	43	100.0	723	6	CA308777 UI-H-FT1
16	43	100.0	723	6	CD368116 UI-H-FT1
17	43	100.0	724	6	CA309711 UI-H-FT1
18	43	100.0	726	6	CA310368 UI-H-FT1
19	43	100.0	726	6	CD368929 UI-H-FT1
20	43	100.0	742	6	CA309509 UI-H-FT1
21	43	100.0	744	6	CD366187 UI-H-FT1
22	43	100.0	748	6	CA306559 UI-H-FT1
23	43	100.0	755	6	CD240146 DTL3P2G5
24	43	100.0	1068	1	AL543083 AL543083

C 25	42	97.7	693	6	CD367625	UI-H-FT1-
C 26	41.4	96.3	672	6	CD367664	UI-H-FT1-
C 27	41.4	96.3	713	6	CA309664	UI-H-FT1-
C 28	41.4	96.3	718	6	CD367794	UI-H-FT1-
C 29	35.2	81.9	581	1	A1242177	qh8g08.x
C 30	33.6	78.1	564	1	AA699697	178f12.8
C 31	28	65.1	561	4	BG232086	raf32e06.
C 32	27.8	64.7	792	7	CK777347	964375 MA
C 33	25	58.1	1011	1	AL575811	AL575811
C 34	24.8	57.7	431	8	A0459761	HS 5125.A
C 35	24.6	57.2	608	6	CB428950	602494 MA
C 36	24	55.3	594	7	N26123	yx90h08.81
C 37	23.8	55.3	163	2	BF737938	CM2-KT003
C 38	23.8	55.3	363	5	BY014887	BY014887
C 39	23.6	54.9	172	2	BF855413	RC4-PN020
C 40	23.6	54.9	545	1	AU260483	AU260483
C 41	23.6	54.9	631	9	CE567682	tigr-g88-
C 42	23.4	54.4	434	6	CB759234	AMGNNUC.N
C 43	23.4	54.4	492	5	BY243201	BY243201
C 44	23.4	54.4	763	5	BQ45871	UI-H-EU1-
C 45	23.4	54.4	2686	3	AK077502	Mus muscu

ALIGNMENTS

RESULT 1
T29839
LOCUS EST97164 Human Testis Homo sapiens cDNA 5' end similar to tumor
DEFINITION necrosis factor, alpha (HT:1190), mRNA sequence.
ACCESSION T29839
VERSION T29839.1 GI:611937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 248)
AUTHORS Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkley P.S., Kelley J.M., Kline K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Dimke D., Feng P., Farrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meissner P.S., Olsen H., Raymond L., Wei Y.-P., Wing J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)
JOURNAL PUBMED 96026280
COMMENT 7566098
Contact: Venter, JC
The Institute for Genomic Research
932 Clippor Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .248

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):107667"
/db_xref="taxon:9606"
/clone_lib="Human Testis"
/note="Organ: testis"

ORIGIN

Query Match 100.0%; Score 43; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 62 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 104
|||||

RESULT 2

LOCUS BX118951 474 bp mRNA linear EST 10-FEB-2003
DEFINITION BX118951 Soares_fetal_heart_NBHL19W Homo sapiens cDNA clone
IMAGE998L124300 ; IMAGE:1693595, mRNA sequence.

ACCESSION

VERSION BX118951.1 GI:27882696

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

Ebert L., Heil O., Hennig S., Neubert P., Partsch E., Peters M.,
Radelof U., Schneider D. and Korn B.

Human Unigeneset - RZPD3

Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE998L124300.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/cloneCards/cgi-

bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACACGGAACACGCTATGAC.

FEATURES

source

Location/Qualifiers

1..474

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE998L124300 ; IMAGE:1693595"

/sex="unknown"

/dev_stages="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal heart NBHL19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site1: Not I; Site2: Eco RI; let

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'];

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by

M.Fatima Bonaldo. This library was constructed from the

same fetus as the fetal lung library, Soares fetal lung

NBHL19W."

ORIGIN

Query Match 100.0%; Score 43; DB 5; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 69 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 111
|||||

RESULT 3

CB528492/c

LOCUS CB528492

DEFINITION CB528492

ACCESSION CB528492

VERSION CB528492.1

KEYWORDS EST.

SOURCE CB528492.1

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 630)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@emil.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 1-29, >AT rich flow complexity (matched complement)

205-279, >(TAAA)nSimple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..630

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT2-bjd-e-20-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stages="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP FT2 is a subtracted cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The mRNA samples

were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of

the conditions, other donor macrophages in different

conditions). The mRNA samples were pooled for library

construction. Control 0 hours; control 3 hours; control 24

hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;

PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella

moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph

aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;

Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;

Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt

adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24

hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;

wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.

The library was subtracted according to Bonaldo, Lennon

and Soares, Genome Research, 6:791-806, 1996. The tissue

was provided by Dr. Gary W. Hunninghake of the University

of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 499 TCAAACTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 457
|||||

RESULT 4

CD370363/c
LOCUS CD370363 645 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bkb-n-03-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
Accession CD370363
Version CD370363.1 GI:31154453
Keywords EST.
Source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 645)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bkb-n-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTL is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV egFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV egFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 645;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
|||||
Db 588 TCAAACTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 546
|||||

RESULT 5

LOCUS

CA307429/c

DEFINITION

CA307429 684 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bic-i-01-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone

ACCESSION

CA307429

VERSION

CA307429.1 GI:24470483

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 684)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bent-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..684
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bic-i-01-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTL is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of

hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
p77T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG_L18=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 684;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43
|||||
Db 591 TCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 549
|||||

RESULT 6

CD367676/c
LOCUS
DEFINITION UI-H-FT1-bjrl-1-14-0-UI-s1 mRNA linear EST 05-AUG-2004
UI-H-FT1-bjrl-1-14-0-UI 3', mRNA sequence.

ACCESSION CD367676.1 GI:31151766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 69-143, >(TAAA)n\$Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjrl-1-14-0-UI"
/tissue_type="Alveolar Macrophage"

FEATURES

source

/dev_stage="Adult"
/lab_hosts="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG_L18=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43
|||||
Db 363 TCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 321
|||||

RESULT 7

CA307225/c
LOCUS
DEFINITION UI-H-FT1-bhu-n-04-0-UI-s1 mRNA linear EST 05-AUG-2004
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.

ACCESSION CA307225
VERSION CA307225.1 GI:24470279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 696)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers

```

1..896
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjm-n-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCGG"

```

ORIGIN

```

Query Match      100.0%; Score 43; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548
|||||

```

RESULT 8

CD364761/c

LOCUS

UI-H-FT2-bjm-j-11-0-UI-s1 NCI CGAP FT2 Homo sapiens cDNA clone

UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.

CD364761

EST.

CD364761.1 GI:31149851

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 699)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

JOURNAL

COMMENT

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation: Dr. Gary W. Hunninghake, U of I
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>

The following repetitive elements were found in this cDNA sequence: 296-370, >(TAAA)n#Simple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..699

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT2-bjm-j-11-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GGCCATGCGG"

ORIGIN

```

Query Match      100.0%; Score 43; DB 6; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548
|||||

```

RESULT 9

CD368142/c

LOCUS

DEFINITION

UI-H-FT1-bjv-e-20-0-UI-s1 NCI CGAP FT1 Homo sapiens cDNA clone

UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.

CD368142

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1..703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-20-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stages="Adult"
/lab_host="NCI CGAP FTL"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dfr)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

FEATURES

Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-14-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stages="Adult"
/lab_host="NCI CGAP FTL"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dfr)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43
|||||
Db 592 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 550
|||||

RESULT 10
CA308256/c
LOCUS
DEFINITION
UI-H-FT1-bjv-e-14-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
UI-H-FT1-bjv-e-14-0-UI 3', mRNA sequence.
CA308256
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

CA308256 713 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bjv-e-14-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
UI-H-FT1-bjv-e-14-0-UI 3', mRNA sequence.
CA308256
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-14-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stages="Adult"
/lab_host="NCI CGAP FTL"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dfr)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dfr)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 713;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCTCCAGAACTCACTGGGCTACAGCTTTGA 43
 |||||
 Db 590 TCAAACCTGGGCTCCAGAACTCACTGGGCTACAGCTTTGA 548

RESULT 11

CB528694/c
 LOCUS
 DEFINITION UI-H-FT2-bjd-1-22-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
 UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.

ACCESSION CB528694
 VERSION
 KEYWORDS
 SOURCE

CB528694.1 GI:29388630

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/cgap.html
 The following repetitive elements were found in this cDNA
 sequence: 294-368, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1..719

Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT2-bjd-1-22-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="NCI CGAP FT2"
 /clone_lib="NCI CGAP FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site1: EcoR I; Site2: Not I;
 NCI CGAP FT2 is a subtracted cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; Control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
 aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
 Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
 Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
 adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
 wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
 The library was subtracted according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. The tissue

was provided by Dr. Gary W. Hunninghake of the University
 of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 719;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACCTGGGCTCCAGAACTCACTGGGCTACAGCTTTGA 43
 |||||
 Db 588 TCAAACCTGGGCTCCAGAACTCACTGGGCTACAGCTTTGA 546

RESULT 12

BQ007008/c

LOCUS

DEFINITION

UI-H-E11-azb-j-22-0-UI.s1 NCI CGAP_E11 Homo sapiens cDNA clone

IMAGE:5846517 3', mRNA sequence.

ACCESSION BQ007008

VERSION BQ007008.1

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1..722

Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5846517"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="NCI CGAP E11"

/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP_E11 is a normalized cDNA library containing the
 following tissue(s): Chondrosarcoma. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 ACACCTGCAC.

TAG_TISSUE=chondrosarcoma

TAG_LIB=UI-H-E11

TAG_SEQ=ACACCTGCAC"

ORIGIN

```

Query Match      100.0%; Score 43; DB 5; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

Db

RESULT 13
CA307062/c
LOCUS
DEFINITION
UI-H-Ft1-bhu-o-04-0-UI.s1 NCI_CGAP_Ft1 Homo sapiens cDNA clone
UI-H-Ft1-bhu-o-04-0-UI 3', mRNA sequence.
ACCESSION
CA307062
VERSION
CA307062.1 GI:24470116
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 295-369, >(TAAA)n$imple_repeat
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES
source
1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ft1-bhu-o-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="NCI CGAP_Ft1"
/clone_lib="NCI CGAP_Ft1"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ft1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,

```

```

digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LTB=UI-H-Ft1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match      100.0%; Score 43; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
589 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 547

Db

RESULT 14
CD364988/c
LOCUS
DEFINITION
UI-H-Ft2-bjn-c-04-0-UI.s1 NCI_CGAP_Ft2 Homo sapiens cDNA clone
UI-H-Ft2-bjn-c-04-0-UI 3', mRNA sequence.
ACCESSION
CD364988
VERSION
CD364988.1 GI:31149078
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n$imple_repeat
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES
source
1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ft2-bjn-c-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="NCI CGAP_Ft2"
/clone_lib="NCI CGAP_Ft2"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ft2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella

```

moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT2

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-05; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0;
QY 1 TCAAACTGGGCTCCAGAACTCACTGGGCTTGA 43
|||||
Db 591 TCAAACTGGGCTCCAGAACTCACTGGGCTTGA 549

RESULT 15

CA308777/c

LOCUS

CA308777 723 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bhy-b-23-0-UI-s1 NCI CGAP_FTI Homo sapiens cDNA clone
UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.

ACCESSION

CA308777

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bentos@iowa.edu

The following repetitive elements were found in this cDNA

sequence: 297-371, >(TAAA)n\$Simple_repeat

Seq primer: M13 FORWARD

POLYA=yes.

Location/Qualifiers

1..723

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT1-bhy-b-23-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP_FTI"

/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a

modified polylinker; Site1: EcoR I; Site2: Not I;

NCI CGAP_FTI is a normalized cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The mRNA samples

were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of

the conditions, other donor macrophages in different

conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage

TAG_LIB=UI-H-FT1

TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.9e-05; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0;
QY 1 TCAAACTGGGCTCCAGAACTCACTGGGCTTGA 43
|||||
Db 591 TCAAACTGGGCTCCAGAACTCACTGGGCTTGA 549

Search completed: September 3, 2005, 02:11:42

Job time : 985.15 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 13:14:57 ; Search time 175.51 Seconds
(without alignments)
400.888 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43

Sequence: 1 tcaactggggccctccagaa.....actgggctacagcttga 43

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	787	US-09-032-297A-13	Sequence 13, Appl
2	43	100.0	787	US-09-229-151C-7	Sequence 7, Appl
3	43	100.0	1585	US-09-023-655-1329	Sequence 1329, Ap
4	43	100.0	1587	US-09-949-016-5156	Sequence 5156, Ap
5	43	100.0	1643	US-08-880-342-36	Sequence 36, Appl
6	43	100.0	1643	US-09-505-250-4	Sequence 4, Appl
7	43	100.0	2270	US-09-229-151C-13	Sequence 13, Appl
8	43	100.0	2570	US-09-229-151C-14	Sequence 14, Appl
9	43	100.0	3634	US-09-166-186-1	Sequence 1, Appl
10	43	100.0	3634	US-09-313-932-1	Sequence 1, Appl
11	43	100.0	3634	US-09-109-663-34	Sequence 34, Appl
12	43	100.0	6582	US-09-949-016-1698	Sequence 1698, A
13	43	100.0	10728	US-09-376-774-5	Sequence 5, Appl
14	23	53.5	11752	US-09-949-016-11756	Sequence 11756, A
15	23	53.5	11865	US-09-949-016-15297	Sequence 15297, A
16	23	53.5	11865	US-09-949-016-15298	Sequence 15298, A
17	23	53.5	33753	US-09-949-016-15741	Sequence 15741, A
18	23	53.5	33756	US-09-949-016-12006	Sequence 12006, A
19	21.4	49.8	601	US-09-949-016-137730	Sequence 137730, A
20	21.4	49.8	601	US-09-949-016-137731	Sequence 137731, A
21	21.4	49.8	1274	US-09-148-545-72	Sequence 72, Appl
22	21.4	49.8	1296	US-09-148-545-126	Sequence 126, Appl
23	21.4	49.8	24707	US-09-740-027-3	Sequence 3, Appl
24	21.4	49.8	24720	US-09-949-016-12341	Sequence 12341, A
25	21.4	49.8	24721	US-09-949-016-15610	Sequence 15610, A
26	21.4	49.8	43133	US-09-949-016-14911	Sequence 14911, A
27	21.4	49.8	99498	US-09-949-016-12621	Sequence 12621, A

28	21.4	49.8	146428	4	US-09-949-016-12620	Sequence 12620, A
29	21.4	49.8	146438	4	US-09-949-016-12081	Sequence 12081, A
30	21	48.8	771	5	PCT-US95-12987-1	Sequence 1, Appl
31	21	48.8	771	5	PCT-US95-12987-3	Sequence 3, Appl
32	21	48.8	771	5	PCT-US95-12987-5	Sequence 5, Appl
33	21	48.8	229354	4	US-09-705-400-64	Sequence 64, Appl
34	21	48.8	636591	4	US-09-949-016-11808	Sequence 11808, A
35	21	48.8	636591	4	US-09-949-016-13388	Sequence 13388, A
36	20.8	48.4	249	4	US-09-513-999C-2202	Sequence 2202, Ap
37	20.8	48.4	285	4	US-09-513-999C-1777	Sequence 1777, Ap
38	20.8	48.4	493	4	US-08-621-976-978	Sequence 978, App
39	20.8	48.4	509	4	US-09-621-976-2765	Sequence 2765, Ap
40	20.8	48.4	534	4	US-09-621-976-714	Sequence 714, App
41	20.8	48.4	601	4	US-09-949-016-51785	Sequence 51785, A
42	20.8	48.4	861	1	US-08-409-731A-1	Sequence 1, Appl
43	20.8	48.4	861	2	US-08-470-298B-1	Sequence 1, Appl
44	20.8	48.4	861	2	US-09-023-073A-1	Sequence 1, Appl
45	20.8	48.4	861	3	US-09-361-737-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boehringer Ingelheim Corporation
; STREET: 900 Ridgebury Road, P.O. Box 368
; CITY: Ridgefield
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06877-0368
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032.297A
; FILING DATE: 27-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038.266
; FILING DATE: 28-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert P. Raymond
; REGISTRATION NUMBER: 25089
; REFERENCE/DOCKET NUMBER: 9/121PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-791-6183

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 787
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: DNA
FEATURE:
NAME/KEY: TNFa 3' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-032-297A-13
Query Match 100.0%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;

```
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
    |||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

Query Match 100.0%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
    |||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 3
US-09-023-655-1329
; Sequence 1329, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
```

```
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9339737
US-09-023-655-1329

Query Match 100.0%; Score 43; DB 4; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
    |||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 4
US-09-949-016-5156
; Sequence 5156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5156
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5156

Query Match 100.0%; Score 43; DB 4; Length 1587;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
    |||||
Db 1009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1051

RESULT 5
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
```

ADDRESSES: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TNF CDNA HSTNFR (EMBL Accession
INDIVIDUAL ISOLATE: #X01394)
FEATURE:
NAME/KEY: CDS
LOCATION: 153..851
US-08-880-342-36

Query Match 100.0%; Score 43; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 6
US-09-505-250-4
Sequence 4, Application US/09505250A
Patent No. 6329148
GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Kao, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:

NAME/KEY: CDS
LOCATION: (153)...(854)
US-09-505-250-4
Query Match 100.0%; Score 43; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 7
US-09-229-151C-13
Sequence 13, Application US/09229151C
Patent No. 6537784
GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 2.0
SEQ ID NO 13
LENGTH: 2270
TYPE: DNA
ORGANISM: Human
FEATURE:
OTHER INFORMATION: chimeric gene : -706TNFPGB3'UTR
US-09-229-151C-13

Query Match 100.0%; Score 43; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1709 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1751

RESULT 8
US-09-229-151C-14
Sequence 14, Application US/09229151C
Patent No. 6537784
GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 2.0
SEQ ID NO 14
LENGTH: 2570
TYPE: DNA
ORGANISM: Human
FEATURE:
OTHER INFORMATION: chimeric gene : -1005TNFPGB3'UTR
US-09-229-151C-14

Query Match 100.0%; Score 43; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 2009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2051
|||||

RESULT 9
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; TITLE: homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||

Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854
|||||

RESULT 10
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes:
; TITLE: structure, homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||

Db 2812 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

RESULT 11

US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-301
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

Db 2812 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

RESULT 12

US-09-949-016-16898
; Sequence 16898, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16898
; LENGTH: 6682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16898

Query Match 100.0%; Score 43; DB 4; Length 6682;
Best Local Similarity 100.0%; Pred. No. 8e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

Db 4103 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 4145

RESULT 13

US-09-376-774-5/c
; Sequence 5, Application US/09376774

; Patent No. 6759236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Gomer, Charles
; APPLICANT: T'Ang, Anne
; TITLE OF INVENTION: Methods To Enhance And Confine Expression
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT APPLICATION NUMBER: US/09/376,774
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 10728
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: recombinant vector pDATH-TNF?
US-09-376-774-5

Query Match 100.0%; Score 43; DB 4; Length 10728;
Best Local Similarity 100.0%; Pred. No. 8.8e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

Db 4216 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 4174

RESULT 14

US-09-949-016-11756
; Sequence 11756, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11756
; LENGTH: 11752
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -- (11752)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11756

Query Match 53.5%; Score 23; DB 4; Length 11752;
Best Local Similarity 74.4%; Pred. No. 13; Mismatches 10; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCT 39

Db 4629 TCCATTTGGGGCTCCAGAGCCACTGGGGCTGCAGGT 4667

RESULT 15

US-09-949-016-15297
; Sequence 15297, Application US/09949016
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15297
; LENGTH: 11865
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11865)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15297
```

```
Query Match          53.5%; Score 23; DB 4; Length 11865;
Best Local Similarity 74.4%; Pred. No. 13;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCT 39
      ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4740 TCCATTGGGGGTCCGAGGCCACTGGGGCCTGCAGGT 4778
```

Search completed: September 2, 2005, 18:55:20
Job time : 177.51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 15:27:57 ; Search time 198.034 Seconds
(without alignments)
1421.994 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaaactgggctccagaa.....actgggctccagctttga 43

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues
Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	43	9	US-09-801-371A-2
2	43	100.0	43	9	US-09-801-371A-2
3	43	100.0	50	9	US-09-801-371A-8
4	43	100.0	81	9	US-09-801-371A-7
5	43	100.0	104	9	US-09-801-371A-1
6	43	100.0	104	9	US-09-801-371A-5
7	43	100.0	787	18	US-10-356-308A-13

8	43	100.0	798	21	US-10-895-393-9	Sequence 9, Appli
9	43	100.0	806	20	US-10-814-634A-5	Sequence 5, Appli
10	43	100.0	1279	16	US-10-247-671-120	Sequence 120, App
11	43	100.0	1585	17	US-10-172-118-501	Sequence 501, App
12	43	100.0	1585	18	US-10-342-887-501	Sequence 501, App
13	43	100.0	1585	18	US-10-641-643-1329	Sequence 1329, Ap
14	43	100.0	1585	20	US-10-370-715B-19	Sequence 19, Appli
15	43	100.0	1643	15	US-10-272-411-4	Sequence 4, Appli
16	43	100.0	1643	15	US-10-218-547-3	Sequence 3, Appli
17	43	100.0	1643	15	US-10-272-328A-4	Sequence 9, Appli
18	43	100.0	1643	15	US-10-310-793-9	Sequence 1901, Ap
19	43	100.0	1643	17	US-10-172-118-1901	Sequence 1901, Ap
20	43	100.0	1643	18	US-10-342-887-1901	Sequence 6, Appli
21	43	100.0	1643	20	US-10-475-024-6	Sequence 1, Appli
22	43	100.0	1643	21	US-10-929-182-1	Sequence 6, Appli
23	43	100.0	1643	22	US-10-475-026-6	Sequence 6, Appli
24	43	100.0	1666	16	US-10-247-671-68	Sequence 68, Appli
25	43	100.0	1669	20	US-10-799-345-17	Sequence 17, Appli
26	43	100.0	1669	20	US-10-688-845-74	Sequence 74, Appli
27	43	100.0	2088	9	US-09-973-850-1	Sequence 1, Appli
28	43	100.0	2088	9	US-09-973-850-2	Sequence 2, Appli
29	43	100.0	2088	9	US-09-973-850-3	Sequence 3, Appli
30	43	100.0	2634	10	US-09-824-322B-1	Sequence 1, Appli
31	43	100.0	2634	10	US-09-932-300-34	Sequence 34, Appli
32	43	100.0	2634	17	US-10-191-997-104	Sequence 104, App
33	43	100.0	2634	18	US-10-202-062-3	Sequence 3, Appli
34	43	100.0	2634	19	US-10-652-795-1	Sequence 1, Appli
35	43	100.0	2634	19	US-10-647-918-1	Sequence 1, Appli
36	43	100.0	2634	21	US-10-770-970-1	Sequence 1, Appli
37	43	100.0	2634	24	US-11-028-780-3	Sequence 3, Appli
38	43	100.0	4830	17	US-10-429-802-33	Sequence 33, Appli
39	43	100.0	4830	17	US-10-430-503-24	Sequence 24, Appli
40	43	100.0	14036	21	US-10-741-600-17806	Sequence 17806, A
41	43	100.0	14769	21	US-10-741-600-18012	Sequence 18012, A
C	42	43	22173	19	US-10-322-696-28	Sequence 28, Appli
43	35	81.4	418	9	US-09-796-692-6223	Sequence 6223, Ap
44	35	81.4	418	14	US-10-040-862-6223	Sequence 6223, Ap
45	35	81.4	418	17	US-10-057-4758-6223	Sequence 6223, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Aeouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801.371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2

Query Match 100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43
|||||

```
Db      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

RESULT 2
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match      100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1

RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match      100.0%; Score 43; DB 9; Length 50;
Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      5 UCAAAACUGGGGCCUCCAGAACACUCACUGGGGCCUACAGCUUGA 47

RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US2002015569A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match      100.0%; Score 43; DB 9; Length 81;
Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      9 UCAAAACUGGGGCCUCCAGAACACUCACUGGGGCCUACAGCUUGA 51

RESULT 5
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match      100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 6
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
```


; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-5

Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 100 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 58
|||||

RESULT 7

US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:

; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,266
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 1 to 787
; OTHER INFORMATION: TNFa 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13
; PAGES: 6361-6373
; DATE: 1985
US-10-356-308A-13

Query Match 100.0%; Score 43; DB 18; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 226 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 268
|||||

RESULT 8

US-10-895-393-9
; Sequence 9, Application US/10895393
; Publication No. US20050048549A1
; GENERAL INFORMATION:
; APPLICANT: CAO, Liangxian
; APPLICANT: MEHTA, Anuradha
; APPLICANT: NARYSHKIN, Nikolai A.
; APPLICANT: PELLEGRINI, Matthew C.

; APPLICANT: ROMFO, Charles M.
; APPLICANT: TRIFILLIS, Panayiota
; APPLICANT: TROTTA, Christopher R.
; TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulat
; FILE REFERENCE: 19025.012
; CURRENT APPLICATION NUMBER: US/10/895,393
; CURRENT FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: PCT/US04/01643
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,637
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-895-393-9

Query Match 100.0%; Score 43; DB 21; Length 798;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 220 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 262
|||||

RESULT 9

US-10-814-634A-5
; Sequence 5, Application US/10814634A
; Publication No. US20040231007A1
; GENERAL INFORMATION:
; APPLICANT: CHENEVAL, Dominique
; APPLICANT: KASTELIC, Tania
; APPLICANT: Novation Pharmaceuticals Inc.
; TITLE OF INVENTION: Assay for Identifying Compounds Which
; TITLE OF INVENTION: Affect Stability of mRNA
; FILE REFERENCE: 793-104CIP
; CURRENT APPLICATION NUMBER: US/10/814,634A
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 09/869,159
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: GB 9828709.7
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-814-634A-5

Query Match 100.0%; Score 43; DB 20; Length 806;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 231 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 273
|||||

RESULT 10

US-10-247-671-120
; Sequence 120, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.

; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 120
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120

Query Match 100.0%; Score 43; DB 16; Length 1279;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 1081 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 1123

RESULT 11
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501

Query Match 100.0%; Score 43; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 1049

RESULT 12
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US2004005840A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.

; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-501

Query Match 100.0%; Score 43; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGA 1049

RESULT 13
US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```
;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match      100.0%; Score 43; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 14
US-10-370-715B-19
; Sequence 19, Application US/10370715B
; Publication NO. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 19
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-19

Query Match      100.0%; Score 43; DB 20; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 15
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication NO. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
```

```
;
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match      100.0%; Score 43; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

Search completed: September 3, 2005, 00:21:56
Job time : 198.034 secs
```

THIS PAGE BLANK (USPTO)